

	Aar85519	Fc epsilon 10	
	Ad101587	Human mut	
	Ad101584	Human imm	
	Ad101584	Fc epsilon 10	
	Ad101589	Human mut	
	Abp60380	Human IgE	
	Aag6559	Amino aci	
	Ad101578	Human imm	
	Ad101593	Human mut	
	Ad101603	Human mut	
	Ad101599	Human mut	
	Ad101601	Human mut	
	Ad101591	Human mut	
	Ad101597	Human mut	
	Aab03643	Rat IgE h	
	Aau80288	Murine IgG	
	Aau80299	Murine IgG	
	Aav79999	Mouse IgB	
	Aav80299	Rat immu	
GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.			
I protein - protein search, using sw model			
on on:	November 14, 2004, 15:03:41 ; Search time 79 Seconds		
	(without alignments)		
	1552.980 Million cell updates/sec		
Title:	US-09-401-636-8		
Perfect score:	1856		
Sequence:	1 EPHHHHHHTLSLPESGPVTTI HEALPGSRTLEKSLHYSGN 342		
Scoring table:	BLOSUM62		
	Gapop 10.0 , Gapext 0.5		
Searched:	2002273 seqs, 358729299 residues		

ALIGNMENTS

RESULT 1						
AAB06205						
AAB06205 standard; protein; 342 AA.						
Database :						
A:	Geneseq23Sep04:*	<				
1:	GeneseqP1980s:*					
2:	GeneseqP1980s:*					
3:	GeneseqP2000s:*					
4:	GeneseqP2001s:*					
5:	GeneseqP2002s:*					
6:	GeneseqP2003as:*					
7:	GeneseqP2003bs:*					
8:	GeneseqP2004s:*					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES						
Result No.	Score	Query Match	Length	DB	ID	Description
1	1856	100.0	342	3	AAB06205	Aab06205 Immunogen
2	1786	96.2	338	8	ADP90025	ADP90025 Opossum-h
3	1786	96.2	338	8	ADn00646	ADn00646 OSO prote
4	1644.5	88.6	341	3	AAB06208	Ab06208 Immunogen
5	1584.5	85.4	341	3	Aab03644	Opossum I
6	1568.5	84.5	341	3	Aab06206	Aab06206 Immunogen
7	1498.5	80.7	337	8	ADP90022	ADP90022 Opossum-r
8	1498.5	80.7	337	8	ADn00643	ADn00643 ORO prote
9	1392.5	75.0	341	3	AAB06202	Aab06202 Immunogen
10	1375	74.1	342	3	AAB06201	Ab06201 Immunogen
11	1038.5	56.0	320	6	AAG19667	Human IgE
12	1038.5	56.0	320	5	AAB08286	Aau08086 Human IgE
13	1038.5	56.0	323	5	AAB08285	Aau08085 Human IgE
14	1029.5	56.0	323	5	AAB08284	Aau08084 Human IgE
15	1038.5	56.0	324	2	AAB83559	Aar83559 Fc (epilo
16	1038.5	56.0	325	2	AAB75225	Aar75225 Human IgE
17	1038.5	56.0	325	2	AAS77241	Human IgE
18	1038.5	56.0	331	3	AAB03642	Human IgE
19	1038.5	56.0	331	7	ADD25768	Binding d
20	1036.5	55.8	330	7	AABU0289	Aau0289 Human IgE
21	1035.5	55.8	325	3	AAY79994	Aay79994 Human imm
22	1019.5	54.9	315	2	AAU080288	Aau080288 Human IgE
23	1019.5	54.9	315	2	AAR85582	Aar85582 Fc (epilo
24	1019.5	54.9	325	2	AAB83582	Aab83582 CH2 to CH
						(Updated on 12-SEP-2003 to standardise OS field)

卷之三

SQ	Sequence 342 AA;	CC	host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided.
	Query Match 100.0%; Score 1856; DB 3; Length 342;	CC	When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
	Best Local Similarity 100.0%; Pred. No. 5.4e-146;	CC	
	Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	CC	
Qy	1 EFPHHHHHTLSLPESGPTTIPPTVKLFHSSCDPGRDAHSTIQQLCLVSGSPAKVHVTW 60	CC	
Db	1 EFPHHHHHTLSLPESGPTTIPPTVKLFHSSCDPGRDAHSTIQQLCLVSGSPAKVHVTW 60	XX	
	Sequence 338 AA;	XX	
		SO	
		Query Match 96.2%; Score 1786; DB 8; Length 338;	
		Best Local Similarity 99.4%; Pred. No. 3.6e-140;	
		Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;	
Qy	9 TLLSPESEGTVLIPPTVLFHSSCDPGRDAHSTIQQLCLVSGSPAKVHVTWLVGQAE 68	Qy	9 TLLSPESEGTVLIPPTVLFHSSCDPGRDAHSTIQQLCLVSGSPAKVHVTWLVGQAE 68
Db	121 KCADSNPRGSVAYLRSRSPFDLFIKSPTITLCLVVDLAPSKGTNLTWSASGVNHSR 120	Db	3 TLLSPESEGTVLIPPTVLFHSSCDPGRDAHSTIQQLCLVSGSPAKVHVTWLVGQAE 62
Qy	121 KCADSNPRGSVAYLRSRSPFDLFIKSPTITLCLVVDLAPSKGTNLTWSASGVNHSR 120	Qy	69 NLFPYTRPKREGQTISLOSEVNITQGMNSNTTCHVRHNGSFEDSSRKCADSNPR 128
Db	121 KCADSNPRGSVAYLRSRSPFDLFIKSPTITLCLVVDLAPSKGTNLTWSASGVNHSR 180	Db	63 NLFPYTRPKREGQTISLOSEVNITQGMNSNTTCHVRHNGSFEDSSRKCADSNPR 122
Qy	181 RKEBKQRNGTLTVTSLPVGTRDWEGETYQCRVTHPLPRAIMSTTKLPGKRLAPEVY 240	Qy	129 GVEAYLSRSPSPFLFIKSPTITLCLVVDLAPSKGTNLTWSASGVNHSRTKEEKQRN 188
Db	181 RKEBKQRNGTLTVTSLPVGTRDWEGETYQCRVTHPLPRAIMSTTKLPGKRLAPEVY 240	Db	123 GVSAYLRSRSPSPFLFIKSPTITLCLVVDLAPSKGTNLTWSASGVNHSRTKEEKQRN 182
Qy	241 MLPPSPPEGTTRTVCLIRGPYPESEISVQWLNFNEEDHTGHHTTRPQDHGTDPSFFL 300	Qy	189 GTLTVTSLPVGTRDWEGETYQCRVTHPLPRAIMSTTKL - PGKRLAPEVYMLPPSP 246
Db	241 MLPPSPPEGTTRTVCLIRGPYPESEISVQWLNFNEEDHTGHHTTRPQDHGTDPSFFL 300	Db	183 GTLTVTSLPVGTRDWEGETYQCRVTHPLPRAIMSTTKLASPGRRLAPEVYMLPPSP 242
Qy	301 YSEMLVNRKSIWEKGNLVIYTCRVVHEALPGSRITLEKSLHYSGN 342	Qy	247 EETGTTTRTVCLIRGPYPESEISVQWLNFNEEDHTGHHTTRPQDHGTDPSFFLYSRLMLV 306
Db	301 YSEMLVNRKSIWEKGNLVIYTCRVVHEALPGSRITLEKSLHYSGN 342	Db	243 EETGTTTRTVCLIRGPYPESEISVQWLNFNEEDHTGHHTTRPQDHGTDPSFFLYSRLMLV 302
	RESULT 2	Qy	307 NKSTWEKGNLVIYTCRVVHEALPGSRITLEKSLHYSGN 342
ADP90025	ADP90025 standard; protein; 338 AA.	Db	303 NKSTWEKGNLVIYTCRVVHEALPGSRITLEKSLHYSGN 338
XX			
AC			
XX			
DT	26-FEB-2004 (First entry)	RESULT 3	
XX		ID ADN0646 standard; protein; 338 AA.	
DE	Opossum-human chimeric IgE polypeptide.	XX	
XX	IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic; autiaasimatic; dermatological.	AC	ADN0646;
XX	Chimeric.	XX	17-JUN-2004 (first entry)
OS	Didelphis virginiana.	XX	DE OSO protein, SEQ ID 6.
OS	Homo sapiens.	XX	KW Antiallergic; vaccine; self-IgE; ORO; OSO; allergy.
PN	WO2003096966-A2.	XX	Synthetic.
XX		XX	
PD	27-NOV-2003.	XX	
XX	XX	PN WO2004022094 A1.	
XX	XX	XX	18-MAR-2004.
XX	XX	XX	02-JUN-2003; 2003WO-IB003075.
PA	(RESI-) RESISTENTIA PHARM AB.	XX	PF 05-SEP-2002; 2002US-0408648P.
XX	Lundgren M, Fuentes A, Magnusson A;	XX	PR (RESI-) RESISTENTIA PHARM AB.
XX	XX	XX	DR PI Hellman LT, Person S, Gansson A;
XX	WPI; 2004-042496/04.	XX	PT WPI; 2004-248376/23.
DR	DR N-PSDB; ADF90024,	XX	PT PT compound, useful for inducing an anti self-IgE antibody response in a mammal for treating or preventing allergies.
XX	XX	XX	XX
PA	New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.	XX	XX
XX	Claim 3; SEQ ID NO 6; 23pp; English.	XX	XX
PS	The present sequence is the protein sequence of an opossum CH2-human CH3-encoding CSO can be used for recombinant production this chimeric IgE in	PS	PS
XX	opossum CH4 (OSO) chimeric IgE polypeptide. A vector comprising DNA encoding CSO	CC	CC

The present invention relates to a composition comprising a polypeptide and an aluminum compound, where the polypeptide comprises a self-IGE polypeptide sequence (e.g., an ORO polypeptide or an OSO polypeptide; / ADN0043, ADN0046, ADN0050, ADN0052, ADN0054, ADN0056, ADN0058 or ADN0061). Administration of the composition to a mammal reduces the level of detectable free IGE in the mammal. The composition is useful for inducing an anti self-IGE antibody response in a mammal for treating or preventing allergies. The present sequence is an OSO protein, used to illustrate the invention. The OSO protein contains an opossum CH2 IGE domain followed by a human CH3 IGE domain followed by an opossum CH4 IGE domain.

The present invention relates to a composition comprising a polypeptide and an aluminum compound, where the polypeptide comprises a self-IgE polypeptide sequence (e.g., an ORO polypeptide or an OSO polypeptide; / ADN0643, ADN0646, ADN0650, ADN0652, ADN0654, ADN0656, ADN0658 or ADN0661). Administration of the composition to a mammal reduces the level of detectable free IgE in the mammal. The composition is useful for inducing an anti self-IgE antibody response in a mammal for treating or preventing allergies. The present protein contains an opossum CH2 IgE domain followed by a human CH3 IgE domain followed by an opossum CH4 IgE domain.

Sequence 338 AA:

Query Match	Score 1786;	DB 8;	Length 338;
Best Local Similarity	96.2%	Pred. No. 3.6-140;	
	99.4%	Q	

Query Match Score 1786; DB 8; Length 338;

Best Local Similarity 99.4%; FreA. NO. 3.6e-140; Mismatches 0; Indels 0; Matches 334; Conservative 0;

9 TLSLPESGPVITIPTVYKLFHSSCDPRGDASHTIQLLCVSGFSPARKVRVTWLVDGQEAE 68

b 3 TLSLPESGPVТИПРТВЛФНССДРГДАХСТІОЛСЛВСГФСАРХТВЛДГQЕА5 62

69	NLFQY-TTPKREGGQINSLQSEVNITOGOMSNTYTCVKHNGSLBEDSSRKCADSNPR	128
63	NLFQYTTBPKREGGQINSLQSEVNITOGOMSNTYTCVKHNGSLBEDSSRKCADSNPR	122

129 GVSAYLRSRSPFPDLFIRKSPTITCLUVVLDAPSKGTVNLTWRSAGKVNHSSTRKEEKQRN 188

123 GVSAYLSSPFDLFIRSETITCLVYDVLAPSKGTVNLITWSRASGKPVNHSRKKEKQRN 182

189 GLLTVTSTLPGVTRDWEGETYQCRVTHPPHLPRALMRSTTKL - PGKRLAPEVYMLPPSP 246

b 183 GTLTVTSTLPVGTRDWEGETYQCRVTHPLPRLMRSTTKLASPGRCLAPEVYMLPPSP 242

Y 247 EETGTTRTVTCLIRGYPSEISVQWLNNNEEHTGHHTTRPQXOHGGTDPSSFFLYSRMLV 306

D 243 EETGQTIVICLIRGFYPSSEISVQWLNFNEEDHTGHHTTTRPQDGHDPSFFLYSRMLV 302
W 307 NKS1MEKGNNIWTGCRYTHAIDGCSPTIYKSHHYSAGN 342

<i>R</i>	303	NKSIWEKGNLVTCRVVHEALPGSRTLEKSSLYSAGN	338
<i>b</i>	303	NKSIWEKGNLVTCRVVHEALPGSRTLEKSSLYSAGN	338

RESULT 4
D. AAB06208 standard. Dose/m. 341 22

AAB06208/
X C

X 12-SEP-2003 (revised)

X T 22-NOV-2000 (first entry)
X P Immunocytic metridia consisting of *Amoea* sp. *CH2*

Dog; opossum; immunoglobulin E; IgE; vaccination; infection; allergy;

asthma; eczema; immunogenic peptide.

Didelphis virginiana.
Canis sp.
Chimæra sp.

WO2000025722-A2.

X D 11-MAY-2000.

X 21-OCT-1999; 99MO-SEE001896.
F

A 02-NOV-1998; 98US-0106652P.
R 22-SEP-1999; 99US-00401336.

X
A (RESI-) RESISTENTIA PHARM AB.

JOURNAL OF POLYMER SCIENCE: PART A

THE IMPERIALIST

XX	DR	WPI; 2000-365342/31.
XX	PT	Immunogenic polypept
XX	PT	immunoglobulin E in
XX	PS	Disclosure; Fig 2; 5
XX	PS	The present Sequence
CC	CC	chain constant region
CC	CC	constant region 3 for
CC	CC	polyclonal anti-self
CC	CC	regions from one member
CC	CC	of different
CC	CC	vaccination in humans
CC	CC	allergies, such as a
CC	CC	(Updated on 12-SEP-2
XX	SQ	Sequence 341 AA;
		Sequence Match
		Best Local Similarity
		Matches 301; Conserva
Qy	1	EFHRRHHHTLIS
Db	1	EFHRRHHHTLIS
Qy	61	LVDGQEAEINLF
Db	61	LVDGQEAEINLF
Qy	121	KCADSNPRGVSY
Db	121	KCSSESDPRGVTY
Qy	181	RKEEKGKRGNTL
Db	180	LNRKHDGFTNL
Qy	241	MLPPSPPEETCT
Db	240	MLPPSPPEETCT
Qy	301	YSRMLVNKSTW
Db	300	YSRMLVNKSTW
		RESULT 5
	ID	AAB03644 standard; p
XX	AC	AAB03644;
XX	DT	22-NOV-2000 (first
XX	DE	Opossum IgB heavy ch
XX	KW	Opossum; immunoglobu
XX	OS	eczema; immunogenic
XX	PX	Didelphis virginiana
PN	PN	WO200025722-A2.
XX	PD	11-MAY-2000.
XX	PF	21-OCT-1999; 99WO
XX	PR	02-NOV-1998; 98US
XX	PR	22-SEP-1999; 99US

WPI: 2000-365342/31.	Immunogenic polypeptides useful for preventing the harmful effects of immunoglobulin E in mammals.		
Disclosure: Fig 2; 50pp; English.	The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the dog. It was shown to cause a stronger polyclonal anti-IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SEP-2003 to standardise OS field)		
Sequence 341 AA:	<table border="0"> <tr> <td style="vertical-align: top;"> <p>Query Match 88.6% ; Score 1644.5; DB 3; Length 341;</p> <p>Best Local Similarity 88.0%; Pred. No. 2 2e-128;</p> <p>Mismatches 17; Conservative 23; Indels 1; Gaps</p> <p>Matches 301;</p> </td><td style="vertical-align: top;"> <p>1 BFFHHHHTLSSLSESGPVTIIPTVKLFHSSCDPREDAAHTSIQLICLVSSGSPAKVHVITW 1 EFHHHHHTLSSLSESGPVTIIPTVKLFHSSCDPREDAAHTSIQLICLVSSGSPAKVHVITW 1 LVDGQEAENLFPPTTRPKREGGQTSQSEENITQGQWMSNTYICHVKNGNSIFEDSSR 61 LVDGQEAENLFPPTTRPKREGGQTSQSEENITQGQWMSNTYICHVKNGNSIFEDSSR 121 KCADSNPRAVASYLSRPPFDLPIRKSPTIILVVDLPIASIGTGVNLITWSRASGKPVNHS 121 KCSSESDPRGATSYLSLSPPSPLDLYVHAKPKITCLVVDLPIATMEG-MNLTWYRESKEPVNPGP 181 RKEKDFHNTITVSTLIVLNNDWIBETTYCRVTHPHLPDVI 180 LNKDFHNTITVSTLIVLNNDWIBETTYCRVTHPHLPDVI 241 MLPPSPEETGTTTVTCIIRGYPSETSVQNLFNNBEDHTGHHTTRPOKEHGTDPSFFL 240 MLPPSPEETGTTTVTCIIRGYPSETSVQNLFNNBEDHTGHHTTRPOKEHGTDPSFFL 301 YSRMLVNSIWERGNLVTCRYTHEALDGSRTLEKSLYHAGN 342 300 YSRMLVNSIWERGNLVTCRYTHEALDGSRTLEKSLYHAGN 341 </p></td></tr> </table>	<p>Query Match 88.6% ; Score 1644.5; DB 3; Length 341;</p> <p>Best Local Similarity 88.0%; Pred. No. 2 2e-128;</p> <p>Mismatches 17; Conservative 23; Indels 1; Gaps</p> <p>Matches 301;</p>	<p>1 BFFHHHHTLSSLSESGPVTIIPTVKLFHSSCDPREDAAHTSIQLICLVSSGSPAKVHVITW 1 EFHHHHHTLSSLSESGPVTIIPTVKLFHSSCDPREDAAHTSIQLICLVSSGSPAKVHVITW 1 LVDGQEAENLFPPTTRPKREGGQTSQSEENITQGQWMSNTYICHVKNGNSIFEDSSR 61 LVDGQEAENLFPPTTRPKREGGQTSQSEENITQGQWMSNTYICHVKNGNSIFEDSSR 121 KCADSNPRAVASYLSRPPFDLPIRKSPTIILVVDLPIASIGTGVNLITWSRASGKPVNHS 121 KCSSESDPRGATSYLSLSPPSPLDLYVHAKPKITCLVVDLPIATMEG-MNLTWYRESKEPVNPGP 181 RKEKDFHNTITVSTLIVLNNDWIBETTYCRVTHPHLPDVI 180 LNKDFHNTITVSTLIVLNNDWIBETTYCRVTHPHLPDVI 241 MLPPSPEETGTTTVTCIIRGYPSETSVQNLFNNBEDHTGHHTTRPOKEHGTDPSFFL 240 MLPPSPEETGTTTVTCIIRGYPSETSVQNLFNNBEDHTGHHTTRPOKEHGTDPSFFL 301 YSRMLVNSIWERGNLVTCRYTHEALDGSRTLEKSLYHAGN 342 300 YSRMLVNSIWERGNLVTCRYTHEALDGSRTLEKSLYHAGN 341 </p>
<p>Query Match 88.6% ; Score 1644.5; DB 3; Length 341;</p> <p>Best Local Similarity 88.0%; Pred. No. 2 2e-128;</p> <p>Mismatches 17; Conservative 23; Indels 1; Gaps</p> <p>Matches 301;</p>	<p>1 BFFHHHHTLSSLSESGPVTIIPTVKLFHSSCDPREDAAHTSIQLICLVSSGSPAKVHVITW 1 EFHHHHHTLSSLSESGPVTIIPTVKLFHSSCDPREDAAHTSIQLICLVSSGSPAKVHVITW 1 LVDGQEAENLFPPTTRPKREGGQTSQSEENITQGQWMSNTYICHVKNGNSIFEDSSR 61 LVDGQEAENLFPPTTRPKREGGQTSQSEENITQGQWMSNTYICHVKNGNSIFEDSSR 121 KCADSNPRAVASYLSRPPFDLPIRKSPTIILVVDLPIASIGTGVNLITWSRASGKPVNHS 121 KCSSESDPRGATSYLSLSPPSPLDLYVHAKPKITCLVVDLPIATMEG-MNLTWYRESKEPVNPGP 181 RKEKDFHNTITVSTLIVLNNDWIBETTYCRVTHPHLPDVI 180 LNKDFHNTITVSTLIVLNNDWIBETTYCRVTHPHLPDVI 241 MLPPSPEETGTTTVTCIIRGYPSETSVQNLFNNBEDHTGHHTTRPOKEHGTDPSFFL 240 MLPPSPEETGTTTVTCIIRGYPSETSVQNLFNNBEDHTGHHTTRPOKEHGTDPSFFL 301 YSRMLVNSIWERGNLVTCRYTHEALDGSRTLEKSLYHAGN 342 300 YSRMLVNSIWERGNLVTCRYTHEALDGSRTLEKSLYHAGN 341 </p>		
ILT 5 J3644 AAB01644 standard; protein; 341 AA.	Opossum IgE heavy chain constant regions 2, 3 and 4. Opossum; immunoglobulin E; IgE; vaccination; infection; allergy; asthmatic eczema; immunogenic peptide. Didelphis virginiana. WO200025722-A2. 11-MAY-2000. 21-OCT-1999; 99NO-SEQ001896. 02-NOV-1998; 98US-0106652P. 22-SEP-1999; 99US-00401636.		
AAB03644, 22-NOV-2000 (first entry)			

OS Rattus sp.
 XX WO/00306966-A2.
 PD 27-NOV-2003.
 XX 15-MAY-2003; 2003WO-IB002503.
 XX 21-MAY-2002; 2002US-0382552P.
 PR (RESI-) RESIDENTIA PHARM AB.
 PA XX
 PA XX
 PA (RESI-) RESIDENTIA PHARM AB.
 PT Lundgren M, Fuentes A, Magnusson A;
 PI Lundgren M, Fuentes A, Magnusson A;
 DR WPI: 2004-042496704.
 DR N-PDSB; ADF90020, ADF90021.
 XX PS
 PT New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or polyadenylation sequence, useful in producing a chimeric IGE polypeptide.
 PT XX
 PS Claim 3; SEQ ID NO 3; 23PP; English.
 XX The present sequence is the protein sequence of an opossum CH2-rat CH3-opossum CH4 (ORO) chimeric IGE polypeptide. A vector comprising a nucleic acid encoding ORO can be used for recombinant production of this chimeric IGE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IGE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IGE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IGE antibody effects of IGE-related diseases such as asthma, allergies and eczema.
 SQ Sequence 337 AA;
 QY 9 TLSLPESGPVITIIPPTVKLFHSSCDPRAHDSTIQLICLVSGFSPAKVHTWLVGDQAE 68
 Db 3 TLSLPESGPVITIIPPTVKLFHSSCDPRAHDSTIQLICLVSGFSPAKVHTWLVGDQAE 62
 QY 69 NLFPYTRPKREGGOTFSLOSEYNTITQGMSSNTYTCVKEKNGSIFEDSSRKCADCNSPR 128
 Db 63 NLFPYTRPKREGGOTFSLOSEYNTITQGMSSNTYTCVKEKNGSIFEDSSRCSDDPR 122
 QY 129 GVSAYLRSRSPFDLIRKSPITIQLVWPLASKGTVNITWSRASGKPVNHSRKKEKORN 188
 Db 123 GVTYLLIPSPDLYENGTPKLICVLNL-ESBNNTTWWERKSIGSASQRSTKHN 181
 QY 189 GTLTVTSTLPGVTRDWEGBTYQCRVTHPLPMLRPTKL - PGKRLAPEVYMLPPSP 246
 Db 182 ATTSTTSILPVDAWDWIESEGYQCRVDIPHFPPIVRSITKLASPGRLAPEVYMLPPSP 241
 QY 247 EETGTTRTVTCIIRGFYPSSEISYQWLNNEEDEHTGHHTTTRPORDHGTDPSFLYSRMLV 306
 Db 242 EETGTTRTVTCIIRGFYPSSEISYQWLNNEEDEHTGHHTTTRPORDHGTDPSFLYSRMLV 301
 QY 307 NKS1WEKGNLVTCRVAHEALPGSRTLEKSLHYAGN 342
 Db 302 NKS1WEKGNLVTCRVAHEALPGSRTLEKSLHYSGN 337
 RESULT 8
 ADN00643
 ID ADN00643 standard; protein; 337 AA.
 AC XX
 DT 17-JUN-2004 (first entry)
 DE ORO protein, SEQ ID 3.
 XX KW Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
 XX OS Synthetic.
 XX XX
 PN WO2004022094-A1.
 XX XX
 PD 18-MAR-2004.
 XX XX
 PF 02-UTN-2003; 2003WO-IB003075.
 XX XX
 PR 05-SEP-2002; 2002US-040648P.
 XX XX
 PA (RESI-) RESIDENTIA PHARM AB.
 PA XX
 PI Hellman LT, Persson S, Gansson A;
 XX XX
 WPI; 2004-248376/23.
 DR N-PDSB; ADN00642.
 XX PT New composition comprising a self-IGE polypeptide and an aluminum compound, useful for inducing an anti self-IGE antibody response in a PT mammal for treating or preventing allergies.
 PT XX
 PS Claim 4; 10BP; English.
 XX The present invention relates to a composition comprising a polypeptide CC and an aluminum compound, where the polypeptide comprises a self-IGE CC polypeptide sequence (e.g. an ORO polypeptide), an OSO polypeptide CC (ADN0643, ADN00646, ADN00650, ADN00654, ADN00656, ADN00658 or CC ADN00661). Administration of the composition to a mammal reduces the CC level of detectable free IGE in the mammal. The composition is useful for CC inducing an anti self-IGE antibody response in a mammal for treating or CC preventing allergies. The present sequence is an ORO protein, used to CC illustrate the invention. The ORO protein contains an opossum CH2 IgE CC domain followed by a rat CH3 IgE domain followed by an opossum CH4 IgE CC domain.
 SQ Sequence 337 AA;
 QY Query Match 80.7%; Score 1498.5; DB 8; Length 337;
 Best Local Similarity 82.4%; Pred. No. 3.1e-116;
 Matches 277; Conservative 20; MisMatches 36; Indels 3; Gaps 2;
 XX
 QY 9 TLSLPESGPVITIIPPTVKLFHSSCDPRAHDSTIQLICLVSGFSPAKVHTWLVGDQAE 68
 Best Local Similarity 82.4%; Pred. No. 3.1e-116;
 Matches 277; Conservative 20; MisMatches 36; Indels 3; Gaps 2;
 QY 9 TLSLPESGPVITIIPPTVKLFHSSCDPRAHDSTIQLICLVSGFSPAKVHTWLVGDQAE 68
 Db 3 TLSLPESGPVITIIPPTVKLFHSSCDPRAHDSTIQLICLVSGFSPAKVHTWLVGDQAE 62
 QY 69 NLFPYTRPKREGGOTFSLOSEYNTITQGMSSNTYTCVKEKNGSIFEDSSRKCADCNSPR 128
 Db 63 NLFPYTRPKREGGOTFSLOSEYNTITQGMSSNTYTCVKEKNGSIFEDSSRCSDDPR 122
 QY 129 GVSAYLRSRSPFDLIRKSPITIQLVWPLASKGTVNITWSRASGKPVNHSRKKEKORN 188
 Db 123 GVTYLLIPSPDLYENGTPKLICVLNL-ESBNNTTWWERKSIGSASQRSTKHN 181
 QY 189 GTLTVTSTLPGVTRDWEGBTYQCRVTHPLPMLRPTKL - PGKRLAPEVYMLPPSP 246
 Db 182 ATTSTTSILPVDAWDWIESEGYQCRVDIPHFPPIVRSITKLASPGRLAPEVYMLPPSP 241
 QY 247 EETGTTRTVTCIIRGFYPSSEISYQWLNNEEDEHTGHHTTTRPORDHGTDPSFLYSRMLV 306
 Db 242 EETGTTRTVTCIIRGFYPSSEISYQWLNNEEDEHTGHHTTTRPORDHGTDPSFLYSRMLV 301
 QY 307 NKS1WEKGNLVTCRVAHEALPGSRTLEKSLHYAGN 342
 Db 302 NKS1WEKGNLVTCRVAHEALPGSRTLEKSLHYSGN 337
 RESULT 9
 AAB06202
 ID AAB06202 standard; protein; 337 AA.
 AC XX
 DT 17-JUN-2004 (first entry)

PS Disclosure; Page 112-113; 151PP; English.

This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for downregulating treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in an *E. Coli* system, this sequence was used to create the epitopes of the invention

Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Indels 7; Gaps 4;

Qy 22 PPIVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPIVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63
Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

Qy 142 LFIRKSPTITCLVVDLAPSKGTVNLTMWSRASKPVNHSRKTRBEEKQNGTITVTSILPVGT 201
Db 124 LFIRKSPTITCLVVDLAPSKGTVNLTMWSRASKPVNHSRKTRBEEKQNGTITVTSILPVGT 183

Qy 202 RDWIEGETTYQCRTVTHPLPRLMRSTTKLPGKRLAPEVYMLPPSPBEETGT -TRVTCI 259
Db 184 RDWIEGETTYQCRTVTHPLPRLMRSTTKLPGKRLAPEVYAF-ATPWNPGGRDKRTIACLI 242

Qy 260 RGFYPSSEISQWLNFEEDHTGHHTTRPQDHGTDPSPFLYSRMLVNKSTWEKGNLVTC 319
Db 243 QNMPMEDISSQVNLTNEVQLPDARSTIQPKTGKSG -GFYFVSRLEVTRAWEQKDEFIC 300

Qy 320 RVHEALFGSRTEBKSLHYSAG 341
Db 301 RAYHEAASSPQTYQRAYSVNPG 322

RESULT 13

AAU80285 standard; protein; 323 AA.
XX AAU80285;
XX DT 30-JUL-2002 (first entry)

Human IgE C2-C3-C4 domains for mammalian expression.
DE 14-MAR-2002.
XX OS Homo sapiens.
OS Synthetic.
XX PN WO200220038-A2.

RESULT 14

AAU80284 standard; protein; 323 AA.
XX AC AAU80284;
XX DT 30-JUL-2002 (first entry)

XX DE Human IgE heavy chain C2-C3-C4 domains.
XX DE Human IgE; allergy; human; antiallergic; immunosuppressive; antianaphylactic;
KW antiasthmatic; dermato logical; antiinflammatory; immunoglobulin E; IgE;
vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;

XX KW heavy chain C domain.

XX OS Synthet ic.

XX DT 05-SEP-2001; 2001WO-DK000579.

XX PR 06-SEP-2000; 2000DK-00001326.

PR 15-SEP-2000; 2000US-0232831P.

XX PA (PHAR-) PHARMEA AS.

XX PI Klynsner S, Von Hoegen P, Volborg B, Gautam A;

XX DR WPI; 2002-383033/41.

N-PSDB; ABK51133.

XX PT Inducing immune response against autologous immunoglobulin E in an animal, by effecting simultaneous presentation of cytotoxic T lymphocyte epitope an/or B-cell epitope derived from the immunoglobulin.

XX PS Disclosure; Page 108-110; 151PP; English.

XX CC This invention relates to a novel method for inducing an immune response against autologous immunoglobulin E (IgE) in an animal. The method comprises effecting simultaneous presentation of cytotoxic T lymphocyte (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell epitope (TH epitope) which is foreign to the animal, by antigen presenting cells (APCs) of the animal's immune system. The epitopes of the invention may be used as a vaccine against allergic diseases. The method of the invention is useful for inducing an immune response against autologous IgE in an animal, which is useful for down-regulating autoimmunity in the animal. This method is useful in the prevention and treatment of allergic diseases such as anaphylaxis, allergic rhinitis, asthma and atopic dermatitis. The present sequence represents the human IgE heavy chain C2-C3-C4 domains optimised for expression in a mammalian system, this sequence was used to create the epitopes of the invention

XX SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
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Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
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SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
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SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

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Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
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SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
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Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
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SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

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Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
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SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

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Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
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SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
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Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
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Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

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Query Match 56.0%; Score 1038.5; DB 5; Length 323;
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Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

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Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

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SQ Sequence 323 AA;

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Best Local Similarity 62.4%; Pred. No. 5.8e-78;
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Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
Matches 201; Conservative 41; Mismatches 73; Indels 4;

Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;
Best Local Similarity 62.4%; Pred. No. 5.8e-78;
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Qy 22 PPTVKLFFISCDPRAHSTIQTLCLVGSFS2AKYRVTWLYDQEAENLFDYTTRPKREG 81
Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

Qy 82 GOTFSLSQSEBNNTQGOMMSNTYTCYKNGSIFEDSSRKACDSNPGRVSAYLSSRSPFID 141
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Db 6 PPTVKILOSSCDGGHHPPTIQLCLVNGYPTGCTINTWLDQYND--VDSLSTASITQE 63

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Db 64 GELASTQSEBLTISQKEWNLSDRTYCQTYQHTFESTKACDSNPGRVSAYLSSRSPFID 123

SQ Sequence 323 AA;

Query Match 56.0%; Score 1038.5; DB 5; Length 323;<

KW	vaccine; anaphylaxis; allergic rhinitis; asthma; atopic dermatitis;	Qy	82 GOTFSI-QOSEVNITOGWMSNTYCHVKHNSIFFDSSRKCADSNPRGVSAYLSPRSPFD 141.
KW	heavy chain C domain.	Db	64 GBLASTSOSLETLQSKEWLSDTYQHTFDSKCDSPRGVSAYLSPRSPFD 123
XX			
OS	Homo sapiens.		
XX			
Key	Location/Qualifiers	Qy	142 LFIRKSDPTTICLUVLDAPSCKTQNLTVWSRASGKPNHSKKEEKGNGLTIVTSFLPGI 201
PH	8.. .note= "IGE heavy chain C2 domain"	Db	124 LFIRKSDPTTICLUVLDAPSCKTQNLTVWSRASGKPNHSKKEEKGNGLTIVTSFLPGI 183
PT	Domain	Qy	100.. .114 RDWIEGETYQCRVTHPHPLALMRSTTKLGKLAPEVNMPPSBETGT.-TRTVTCL 259
PT	/note= "Epitope including C2C3 linker"	Db	184 RDWIEGETYQCRVTHPHPLALMRSTTKLGKLAPEVNMPPSBETGT.-TRTVTCL 242
Region	104.. .111		
PT	/note= "Linker between domains C2 and C3"	Qy	202 RDWIEGETYQCRVTHPHPLALMRSTTKLGKLAPEVNMPPSBETGT.-TRTVTCL 319
PT	Domain	Db	184 RDWIEGETYQCRVTHPHPLALMRSTTKLGKLAPEVNMPPSBETGT.-TRTVTCL 319
PT	/label= IGE heavy chain C3 domain	Qy	260 RGFPYSEISYQWLNFNEEDHTGHFTTRPQDHDGNDPSFFLYSRMLVNSIWEKNLVTC 319
PT	112.. .211	Db	243 QNMPMPEDISYQWLNEVQLDPARHSTIQPKTKGS.-GFPVFSRLEVTRAEEQXDEFIC 300
Region	139.. .145		
PT	/note= "Epitope in BC loop"	Qy	320 RVVHEALPGSRTEKSLHYSG 341
PT	167.. .175	Db	301 RAVHEAASPOTVQRAVSVNPG 322
Region	210.. .218		
PT	Domain	Qy	
PT	196.. .206	Db	
Region	212.. .218		
PT	/note= "Epitope in DE loop"	Qy	
PT	212.. .215	Db	
Region	216.. .317		
PT	/note= "Epitope including C3C4 linker"	RESULT 15	
PT	Domain	AAR83559	
PT	212.. .215	ID	AAR83559 standard; protein; 324 AA.
XX		XX	
XX		AC	AAR83559;
XX		XX	06-MAR-1996 (first entry)
XX		DT	
XX		XX	DE Fc (epsilon) CH ₂ ' -CH ₄ protein sequence.
XX		XX	FC (epsilon); antibody; human; myeloma; probe; IgE; tryptophan promoter;
XX		XX	constant heavy region; E.coli; Glycosylation; antigenic; immunogenic;
XX		XX	histamine; anti-allergenic; vaccine; immune response.
XX		XX	Synthetic.
XX		XX	OS
XX		XX	FR2715304-A1.
XX		XX	PN FR2715304-A1.
XX		XX	PD 28-JUL-1995.
XX		XX	PF 26-JAN-1994;
XX		XX	PF 94FR-00000846.
XX		XX	PR 26-JUN-1994;
XX		XX	PR 94FR-00000846.
PA	(PHAR-X) PHARMAXA AS.	PA	(INMR) PASTEUR MERLEUX SERUMS & VACCINS.
XX		XX	
XX		XX	PI Hurpin CM, Panero NM;
XX		XX	XX WPI; 1995-265243/35.
XX		XX	DR N-PSDB; AAT01865.
XX		XX	Antiallergic vaccine contg. polypeptide fragment of IgE heavy chain - has PT epitope(s) not present in native IgE, also derived antibodies for PT treating or preventing allergies, inflammatory disease, etc.
XX		XX	CC The amino acid sequence of the Fc(epsilon) CH ₂ '-CH ₄ fragment covering CC amino acids 236-547. The DNA sequence was isolated from a human myeloma CC 266BL cDNA library screened with a probe correspong to the N-terminus of CC IgE. The region encoding amino acids 218-547 was cloned into the vector CC pWT21 under control of the tryptophan promoter. The resultant protein CC produced contains some non-Fc amino acids. These were removed by CC replacing their coding sequence with a bicistrionic linker. The resultant CC construct encodes the Fc(epsilon) constant heavy region from amino acids CC 226-547. When it is expressed in E.coli, the protein produced is a non- CC glycosylated Fc(epsilon) fragment. Altering the pattern of glycosylation CC unmasks new antigenic sites thus rendering the Fc fragment immunogenic CC and able to induce antibodies that recognise native IgE but do not form CC histamine-releasing complexes. The Fc fragments can be used in anti- CC allelgenic vaccines to modulate the intensity of immune responses CC mediated by IgE
XX		XX	
XX		XX	PS Claim 3: Page 32-33; 44pp; French.
XX		XX	XX
CC	This invention relates to a novel method for inducing an immune response CC against autologous immunoglobulin E (IgE) in an animal. The method CC comprises effecting simultaneous presentation of cytotoxic T lymphocyte CC (CTL) epitope and/or B-cell epitope derived from IgE, and T helper cell CC epitope (TH epitope) which is foreign to the animal, by antigen CC presenting cells (APCs) of the animal's immune system. The epitopes of CC the invention may be used as a vaccine against allergic diseases. The CC method of the invention is useful for inducing an immune response against CC autologous IgE in an animal. This method is useful in the prevention and CC treatment of allergic diseases such as anaphylaxis, allergic rhinitis, CC asthma and atopic dermatitis. The present sequence represents the human CC IgE heavy chain C2-C3-C4 domains used to create the epitopes of the CC invention		
XX		XX	XX
SQ	Sequence 323 AA;	XX	
Query Match	56.0%	Score 1038.5;	DB 5; Length 323;
Best Local Similarity	62.4%	Pred. No. 5.3e-7;	
Matches 201; Conservative	41;	Mismatches 73;	Indels 7; Gaps 4;
Qy	22 PPVYKLQSSCDPGDAIISTIQLICLGVGFSPAKVAVLVDQEAENLFPTKREG 81		
Db	6 PPVYKLQSSCDPGDAIISTIQLICLGVGFSPAKVAVLVDQEAENLFPTKREG 81		

XX	Sequence 324 AA;	Score 1038.5;	DB 2;	Length 324;
	Query Match	56.0%;	Pred. No. 5.8e-78;	
	Best Local Similarity	62.4%;	Mismatches 73;	Indels 7; Gaps 4;
	Matches 201; Conservative	41;		
Qy	22 PPTVKLFHSSCDPRGDAHSTIQCLICVNGFSPAKHYTWLYDQEAENLFFPYTRPKREG	81		
Db	7 PPTVKILQSCDGGHFPPTIQCLICVSGTGTINITWLEQYMD--VDLSTATTC	64		
Qy	82 GQFPLSQSVNITQGQWISNVTCTCVAHNGSIFEDSRKCADSNRQGDSAYLSRSPFD	141		
Db	65 GELASTQSEPLTSQKHWLSDRYTCQVY QHTFEDSTKCADSNRQGVSAYLSRSPFD	124		
Qy	142 LFIRKSPTITCLVYDLPASKGTVNLWMSRASKPVNHSSTRKEKQNGTIVTSLPVG	201		
Db	125 LFIRKSPTITCLVYDLPASKGTVNLWMSRASKPVNHSSTRKEKQNGTIVTSLPVG	184		
Qy	202 RDWIEGETYQCRYTHPHLPRALMRSITKLPGKRLAPEVYMLPSPEETGT -TRIVTCI	259		
Db	185 RDWIEGETYQCRYTHPHLPRALMRSITKLPGKRLAPEVYAF ATPEWGSDEKTIACI	243		
Qy	260 RGFYPSEISQWLNNEEDHTGHHTTRPOKHGTDPSEFLYSRMLYNKSIWEKGNLVTC	319		
Db	244 QNFMPEDISQWLNHEVOLPDARHSTIOPRKTKGS--GFFVFSRLEVTRAWEQKDEFIC	301		
Qy	320 RVVHBALPQSRTEKSLHYSA	341		
Db	302 RAVHEAAASQCTYGRAVSNPG	323		

Search completed: November 14, 2004, 15:06:52
 Job time : 61 secs

GenCore version 5.1.6
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OM protein - protein search, using sw mode!

Run on: November 14, 2004, 15:06:56 ; Search time 79 Seconds

(without alignments)

1531.723 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence: 1 EFPHHHHHTLSSLPPSGPVTHI.....HEALPGSRTLEKSLHYSGAGN 342

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters:

1219554

Minimum DB seq length: 0

Maximum DB seq length: 342

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing First 45 summaries

Database :

Published Applications AA:
 1: /cggn2_6/ptodata/1/pubpaas/us007_PUBCOMB.pep;*

2: /cggn2_6/ptodata/1/pubpaas/us007_PUBCOMB.pep;*

3: /cggn2_6/ptodata/1/pubpaas/us006_NEWPUB.pep;*

4: /cggn2_6/ptodata/1/pubpaas/us006_PUBCOMB.pep;*

5: /cggn2_6/ptodata/1/pubpaas/us007_NEWPUB.pep;*

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7: /cggn2_6/ptodata/1/pubpaas/us008_NEWPUB.pep;*

8: /cggn2_6/ptodata/1/pubpaas/us009A_PUBCOMB.pep;*

9: /cggn2_6/ptodata/1/pubpaas/us009B_PUBCOMB.pep;*

10: /cggn2_6/ptodata/1/pubpaas/us010A_PUBCOMB.pep;*

11: /cggn2_6/ptodata/1/pubpaas/us009C_PUBCOMB.pep;*

12: /cggn2_6/ptodata/1/pubpaas/us010A_PUBCOMB.pep;*

13: /cggn2_6/ptodata/1/pubpaas/us10A_PUBCOMB.pep;*

14: /cggn2_6/ptodata/1/pubpaas/us10B_PUBCOMB.pep;*

15: /cggn2_6/ptodata/1/pubpaas/us10C_PUBCOMB.pep;*

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17: /cggn2_6/ptodata/1/pubpaas/us10D_NEWPUB.pep;*

18: /cggn2_6/ptodata/1/pubpaas/us11_NEWPUB.pep;*

19: /cggn2_6/ptodata/1/pubpaas/us11_NEWPUB.pep;*

20: /cggn2_6/ptodata/1/pubpaas/us60_NEWPUBCOMB.pep;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES

Result No. Score Query Match Length DB ID Description

Result No.	Score	Query	Match	Length	DB ID	Description
1	1856	100.0	342	9	US-09-401-636-8	Sequence 8, Appli
2	1856	100.0	342	14	US-10-176-664-8	Sequence 8, Appli
3	1856	100.0	342	15	US-10-173-594-8	Sequence 8, Appli
4	1786	96.2	338	15	US-10-138-724-6	Sequence 6, Appli
5	1786	96.2	338	15	US-10-153-915-6	Sequence 6, Appli
6	1644.5	88.6	341	9	US-09-401-636-11	Sequence 11, Appli
7	1644.5	88.6	341	14	US-10-176-664-11	Sequence 11, Appli
8	1644.5	88.6	341	15	US-10-613-594-11	Sequence 11, Appli
9	1587.5	85.5	341	9	US-09-401-636-3	Sequence 3, Appli
10	1587.5	85.5	341	14	US-10-176-664-3	Sequence 3, Appli
11	1587.5	85.5	341	15	US-10-613-594-3	Sequence 3, Appli
12	1587.5	84.5	341	9	US-09-401-636-9	Sequence 9, Appli
13	1588.5	84.5	341	14	US-10-176-664-9	Sequence 9, Appli

RESULT 1	US-09-401-636-8	Query Match	100.0% ; PRED. NO. 1.5E-139 ; LENGTH 342;
		Best Local Similarity	100.0% ; Mismatches 0 ; Indels 0 ; Gaps 0 ;
		Matches 342 ; Conservative	
		Qy	1 EFHHHHHHHTLSSLPSGPVTHIPPTVKLPHSSCDPRGDAHSTIQLLCLVSGFSPAKVNTW
		Db	1 EFHHHHHHHTLSSLPSGPVTHIPPTVKLPHSSCDPRGDAHSTIQLLCLVSGFSPAKVNTW
		Qy	61 LVDGQAENIFPYTRPKREGQTFSLOSEVNITQGOMSNNTYTCVXKHNSIPEFDSR 120
		Db	61 LVDGQAENIFPYTRPKREGQTFSLOSEVNITQGOMSNNTYTCVXKHNSIPEFDSR 120
		Qy	121 KCADSNPRGVSYAISRPSPDLFIRKSPRITCLVDSLPSKGIVNLWMSRASGRVNST 180

ALIGNMENTS

Sequence 9, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 6, Appli
14 1568.5 84.5	15 1553.5 83.7	14 1553.5 83.7	14 1553.5 83.7	15 1553.5 83.7
15 1568.5 84.5	16 1553.5 83.7	17 1553.5 83.7	18 1528.5 82.4	19 1528.5 82.4
15 1568.5 84.5	16 1553.5 83.7	17 1553.5 83.7	18 1528.5 82.4	19 1528.5 82.4
20 1528.5 82.4	21 1519 81.8	22 1519 81.8	23 1519 81.8	24 1498.5 80.7
20 1528.5 82.4	21 1519 81.8	22 1519 81.8	23 1519 81.8	24 1498.5 80.7
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RESULT 2
US-10-176-664-8

Sequence 8 Application US/10176664
Publication No. US20030031663A1

GENERAL INFORMATION:
 APPLICANT: Hellman, Lars T.
 TITLE OF INVENTION: ENHANCED VACCINES
 FILE REFERENCE: 10223/006001
 CURRENT FILING DATE: 2003-09-29
 PRIORITY APPLICATION NUMBER: US/09/401,636
 PRIOR FILING DATE: 1999-09-22
 PRIORITY APPLICATION NUMBER: US 60/106,652
 PRIOR FILING DATE: 1998-11-02
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8
 LENGTH: 342
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetically generated proteins
 US-10-673-594-8

Query Match 100.0%; Score 1856; DB 15; Length 342;
 Best Local Similarity 100.0%; Pred. No. 1.5e-139;
 Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFPHHHHHTLSLPESGPTTIIPTVKLFHSSCDPRAAHSTIQLLLVGSPAKVHVTW 60
 Db 1 EFPHHHHHTLSLPESGPTTIIPTVKLFHSSCDPRAAHSTIQLLCVSGFSPAKVHVTW 60

Qy 61 LYDGQEAEANLFPTTTRKREGGOTFSILOSEYNTITOGWMSSNTYCHVRNGSIFEDSSR 120
 Db 61 LYDGQEAEANLFPTTTRKREGGOTFSILOSEYNTITOGWMSSNTYCHVRNGSIFEDSSR 120

Qy 121 KCADSNPRGVASYLSRSPFDLFIKSPTTICLVYDIAPIASGKPVNHST 180
 Db 121 KCADSNPRGVASYLSRSPFDLFIKSPTTICLVYDIAPIASGKPVNHST 180

Qy 121 KCADSNPRGVASYLSRSPFDLFIKSPTTICLVYDIAPIASGKPVNHST 180
 Db 121 KCADSNPRGVASYLSRSPFDLFIKSPTTICLVYDIAPIASGKPVNHST 180

Qy 181 RKEEKQNGTITVTTLPVGTBDWIEGETYQCRVTHPLPRLMRSTKLPGRKLAPENVY 240
 Db 181 RKEEKQNGTITVTTLPVGTBDWIEGETYQCRVTHPLPRLMRSTKLPGRKLAPENVY 240

Qy 241 MPPSPBETGTTRTVCILRGYPSEISVONLFNNEDHTGHHTTRPKDHGTDPSFFL 300
 Db 241 MPPSPBETGTTRTVCILRGYPSEISVONLFNNEDHTGHHTTRPKDHGTDPSFFL 300

Qy 241 MPPSPBETGTTRTVCILRGYPSEISVONLFNNEDHTGHHTTRPKDHGTDPSFFL 300
 Db 241 MPPSPBETGTTRTVCILRGYPSEISVONLFNNEDHTGHHTTRPKDHGTDPSFFL 300

RESULT 4
US-10-438-794-6

Sequence 6 Application US/10438794
Publication No. US20040038395A1

GENERAL INFORMATION:
 APPLICANT: Fuentes, Alexis
 APPLICANT: MAGNUSSON, Ann-Christin
 TITLE OF INVENTION: Chimeric IgE Peptides and Host Cells
 FILE REFERENCE: 10223/017001
 CURRENT APPLICATION NUMBER: US/10/438-794
 CURRENT FILING DATE: 2003-05-15
 PRIORITY APPLICATION NUMBER: US 60/382,552
 PRIOR FILING DATE: 2002-05-21
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 6
 LENGTH: 338
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic polypeptide designated OSO
 US-10-438-794-6

Query Match

RESULT 3
US-10-673-594-8

Sequence 8 Application US/10673594
Publication No. US004007662A1

GENERAL INFORMATION:

Best Local Similarity 99.4%; Pred. No. 5_7e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 9 TLSPESGVFTIIPPTVLFHSSCDPRAHSTIQLCLVSGSPARVHTWLVQDQAE 68
Db 3 TLSPESGVTIIPPTVLFHSSCDPRAHSTIQLLVSGSPARVHTWLVQDQAE 62

Qy 69 NLFPYTRPKREGQTFSIQSEYNTIQQWMSNTYCHVKINGSIPEFDSRKCADSNPR 128
Db 63 NLFPYTRPKREGQTFSIQSEYNTIQQWMSNTYCHVKINGSIPEFDSRKCADSNPR 122

RESULT 6
US-09-401-636-11
; Sequence 11, Application US/09401636
; GENERAL INFORMATION:
; Application: Hellman, Lars T.
; Title of Invention: ENHANCED VACCINES
; File Reference: 10223/000001
; Current Application Number: US/09/401,636
; Current Filing Date: 1993-09-22
; Prior Application Number: US 60/106,652
; Prior Filing Date: 1998-11-02
; Number of SEQ ID NOS: 11
; Software: FastSEQ for Windows Version 4.0
; SEQ ID NO: 11
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated proteins
; US-09-401-636-11

Query Match 88 6%; Score 1644,5; DB 9; Length 341;
Best Local Similarity 88.0%; Pred. No. 1.e-122;
Matches 301; Conservative 17; Mismatches 23; Indexes 1; Gaps 1;

Qy 1 EFHHHHHTLSPESGPVIIIPPTVKLHSSCDPRAHSTIQLCLVSGSPAKVHTW 60
Db 1 EFHHHHHTLSPESGPVIIIPPTVKLHSSCDPRAHSTIQLCLVSGSPAKVHTW 60

Qy 61 LVDGGEAENLPYTRPKREGQTFSQLEVNITQGOMSNTYCHVKHNGSLFDSSR 120
Db 61 LVDGGEAENLPYTRPKREGQTFSQLEVNITQGOMSNTYCHVKHNGSLFDSSR 120

Qy 121 KCADNPNGSYAISRPSPDLFRKSPVITLVDLAPSKGTVNLTVRSASGPVNHT 180
Db 121 KCSEDPRGYTSVLSPPSPDLYTHAKPITCLVLDATMBEG-MNLTIVRESKPVNCP 179

Qy 181 RKEEKFONGLTVTSLPVGTRDWLGEETYOCRTHPHLPRALMRSTTKLGKRLAPEVY 240
Db 180 LNKDHFGNTITVSLPVGTRDWLGEETYOCRTHPHLPRALMRSTTKLGKRLAPEVY 239

Qy 241 MLPPSPPEETGTTRTVCLRGFYESEISQWLNNEEDHTGHHTTRQKDHGTDPSFPL 300
Db 240 MLPPSPPEETGTTRTVCLRGFYESEISQWLNNEEDHTGHHTTRQKDHGTDPSFPL 299

RESULT 7
US-10-10453-915-6
; Sequence 11, Application US/10453915
; Publication No. US20040054146A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; APPLICANT: Persson, Stefan
; APPLICANT: Jansson, Asa
; TITLE OF INVENTION: Allergy Vaccines
; FILE REFERENCE: 10223/008001
; CURRENT APPLICATION NUMBER: US/10/453,915
; PRIOR APPLICATION NUMBER: 2003-06-02
; PRIOR FILING DATE: 2002-09-05
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 338
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: chimeric polypeptide
; US-10-453-915-6

Query Match 96.2%; Score 1786; DB 15; Length 338;
Best Local Similarity 99.4%; Pred. No. 5_7e-134;
Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 9 TLSPESGVFTIIPPTVLFHSSCDPRAHSTIQLCLVSGSPARVHTWLVQDQAE 68
Db 3 TLSPESGVTIIPPTVLFHSSCDPRAHSTIQLCLVSGSPARVHTWLVQDQAE 62

Qy 69 NLFPYTRPKREGQTFSIQSEYNTIQQWMSNTYCHVKINGSIPEFDSRKCADSNPR 128
Db 63 NLFPYTRPKREGQTFSIQSEYNTIQQWMSNTYCHVKINGSIPEFDSRKCADSNPR 122

Qy 129 GVSAYLSPSPSPDFLFRKSPVITLVDLAPSKGTVNLTVRSASGPVHTKERN 188
Db 123 GVSAYLSPSPSPDFLFRKSPVITLVDLAPSKGTVNLTVRSASGPVHTKERN 182

Qy 189 GTLTVTSVPVGDRWIGETQCRVTPHLPALEMSTKL--PGKRLAPEVMLPPSP 246
Db 183 GTLTVTSVPVGDRWIGETQCRVTPHLPALEMSTKLASPGKRLAPEVMLPPSP 242

Qy 247 EETGTRTVCLRGFYESEISQWLNNEEDHTGHHTTRQKDHGTDPSFFLYSRMLV 306
Db 303 NRSIWEKGNLVTCRVHEALPGSRTLEKSLHYSGN 338

NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FastSEQ for Windows version 4.0
 SEQ ID NO: 11
 LENGTH: 341
 TYPE: PRY
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetically generated proteins
 US-10-176-636-11

Query Match 88.6%; Score 1644.5; DB 14; Length 341;
 Best Local Similarity 88.0%; Pred. No. 1..1e-122;
 Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

Db 61 LVDQEAENLFPPTTRPKREGQTFSQSEYNITQGMSSNTYCHVKINGSIFEDSSR 120
 Qy 121 KCADSNPFGVSAYLSPRSPFDLPIRKSPITCLVVDIAPSKGTVNLTWSASGKPVNHST 180
 Db 121 KCSESDPFGVTSYLSPSPDLYVHAKPKTCIQLVVDIATMEG-MNLTWYBESKEPNPGP 179
 Qy 181 RKEEKQRNGTLLTVTSTLPVGTRDWEGETYQCRVTHPHLPRALMRSITKLPGKRLAPEVY 240
 Db 180 LNKKDHFNFTTVTSTLPVNTNDWIEETTYQCRVTHPLPDIVRIIAKLPGKRLAPEVY 239
 Qy 1 EPHHHHHHTLSLPSFGPTTIPPTVKLFPHSSCDPGRDAHSTIQLCIVSFSPARKVHWTW 60
 Db 1 EPHHHHHHTLSLPSFGPTTIPPTVKLFPHSSCDPGRDAHSTIQLCIVSFSPARKVHWTW 60
 Qy 61 LVDQEAENLFPPTTRPKREGQTFSQSEYNITQGMSSNTYCHVKINGSIFEDSSR 120
 Db 61 LVDQEAENLFPPTTRPKREGQTFSQSEYNITQGMSSNTYCHVKINGSIFEDSSR 120
 Qy 121 KCADSNPFGVSAYLSPRSPFDLPIRKSPITCLVVDIAPSKGTVNLTWSASGKPVNHST 180
 Db 121 KCSESDPFGVTSYLSPSPDLYVHAKPKTCIQLVVDIATMEG-MNLTWYBESKEPNPGP 179
 Qy 181 RKEEKQRNGTLLTVTSTLPVGTRDWEGETYQCRVTHPHLPRALMRSITKLPGKRLAPEVY 240
 Db 180 LNKKDHFNFTTVTSTLPVNTNDWIEETTYQCRVTHPLPDIVRIIAKLPGKRLAPEVY 239
 Qy 241 MLPPSPERTGTTTVTCLRGFYPESETSVQWLNNEEDHTGHHTTRPQKDHTDPSFFL 300
 Db 240 MLPPSPERTGTTTVTCLRGFYPESETSVQWLNNEEDHTGHHTTRPQKDHTDPSFFL 299
 Qy 301 YSRMLVNRKSIWERGNLYTCRVNLVTCRVHEALPGSRTLEKSILHYSGN 342
 Db 300 YSRMLVNRKSIWERGNLYTCRVNLVTCRVHEALPGSRTLEKSILHYSGN 341
 Db 300 YSRMLVNRKSIWERGNLYTCRVNLVTCRVHEALPGSRTLEKSILHYSGN 341

RESULT 9
 US-09-401-636-3
 Sequence 3; Application US/09401636
 ; Patent No. US2001038843A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hellman, Lars T.
 ; TITLE OF INVENTION: ENHANCED VACCINES
 ; FILE REFERENCE: 10/23/006001
 ; CURRENT APPLICATION NUMBER: US/09/401-636
 ; CURRENT FILING DATE: 1999-09-22
 ; PRIOR APPLICATION NUMBER: US 60/106,652
 ; PRIOR FILING DATE: 1998-11-02
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 3
 ; LENGTH: 341
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetically generated proteins
 US-09-401-636-3

Query Match 85.5%; Score 1587.5; DB 9; Length 341;
 Best Local Similarity 85.4%; Pred. No. 3..8e-118;
 Matches 28; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

Db 1 EPHHHHHHTLSLPSFGPTTIPPTVKLFPHSSCDPGRDAHSTIQLCIVSFSPAKVHWTW 60
 Qy 1 EPHHHHHHTLSLPSFGPTTIPPTVKLFPHSSCDPGRDAHSTIQLCIVSFSPAKVHWTW 60
 Db 1 EPHHHHHHTLSLPSFGPTTIPPTVKLFPHSSCDPGRDAHSTIQLCIVSFSPAKVHWTW 60
 Qy 121 KCADSNPREGISAYLSPRSPFDLPIRKSPITCLVVDIAPSKGTVNLTWSASGKPVNHST 180
 Db 121 KCSPDTDPRGISAYLPPQDLFVKKPTGCLVVDIAPSKGTVNLTWSASGKPVNHST 179
 Qy 181 RKEEKQRNGTLLTVTSTLPVGTRDWEGETYQCRVTHPHLPRALMRSITKLPGKRLAPEVY 240
 Db 180 LVVKEQINGTFTTSHLPVNTDWIGDTYCRLESDDMPVPLRTSKAFGKRLAPEVY 239
 Qy 241 MLPPSPERTGTTTVTCLRGFYPESETSVQWLNNEEDHTGHHTTRPQKDHTDPSFFL 300
 Db 240 MLPPSPERTGTTTVTCLRGFYPESETSVQWLNNEEDHTGHHTTRPQKDHTDPSFFL 299
 Qy 301 YSRMLVNRKSIWERGNLYTCRVNLVTCRVHEALPGSRTLEKSILHYSGN 342
 Db 300 YSRMLVNRKSIWERGNLYTCRVNLVTCRVHEALPGSRTLEKSILHYSGN 341
 RESULT 10
 US-10-176-664-3
 ; Sequence 3; Application US/10176664

Publication No. US20030031663A1

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US/10/176, 664

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106, 652

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 3

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically generated proteins
US-10-176-664-3

Query Match Score 1587.5; DB 15; Length 341;

Best Local Similarity 85.4%; Pred. No. 3.8e-118;

Matches 292; Conservative 21; Mismatches 28; Indels 1; Gaps 1;

Qy 1 EFPHHHHHTLSPSGPVTIIPPTVKLPHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60

Db 1 EFPHHHHHTLSPSGPVTIIPPTVKLPHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60

Qy 61 LVDGGEAENLFPTTRKREGQTFSLOSEVNITQGMNSNTYTCYKHNGSIFEDSSR 120

Db 61 LVDGGEAENLFPTTRKREGQTFSLOSEVNITQGMNSNTYTCYKHNGSIFEDSSR 120

Qy 121 KCADSNPVGSAVLSPSPFDLIRKSPTITCLVVDLAPSKGTVNLTMRSASSKPVNHS 180

Db 121 KCSDPDPRGISAATLPPQDLPVKVETIGLIVDIA-SAENVKIVSRESGGPVNSS 179

Qy 61 LVDGGEAENLFPTTRKREGQTFSLOSEVNITQGMNSNTYTCYKHNGSIFEDSSR 120

Db 61 LVDGGEAENLFPTTRKREGQTFSLOSEVNITQGMNSNTYTCYKHNGSIFEDSSR 120

Qy 121 KCADSNPVGSAVLSPSPFDLIRKSPTITCLVVDLAPSKGTVNLTMRSASSKPVNHS 180

Db 121 KCSDPDPRGISAATLPPQDLPVKVETIGLIVDIA-SAENVKIVSRESGGPVNSS 179

Qy 181 RKEEKQNGTLYTSTLPGTRDWTIEGETYQCRVTHPHPLRALMRSTTKLPGRLAPEVY 240

Db 180 LYVKEQYNGTFTVSHLVNTDWDIEGTYTCTRLESDMPVBLIRTSKAPKRLAPEVY 239

Qy 241 MLPPSPETGTTRVTCIIRGYFPESEISQWLNFNEEDHTGHHTTRPQDHGHTDPSFL 300

Db 240 MLPPSPETGTTRVTCIIRGYFPESEISQWLNFNEEDHTGHHTTRPQDHGHTDPSFL 299

Qy 301 YSRMLVNKSIWEKGNLVTCRVHEALPGSRTRLEKSLHYSGN 342

Db 300 YSRMLVNKSIWEKGNLVTCRVHEALPGSRTRLEKSLHYSGN 341

RESULT 12

US-09-401-636-9

Sequence 9, Application US/09401636

Patent No. US20030038843A1

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/09/401, 636

PRIOR APPLICATION NUMBER: 1998-09-22

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 9

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-9

Query Match Score 1568.5; DB 9; Length 341;

Best Local Similarity 83.3%; Pred. No. 1.2e-116;

Matches 285; Conservative 20; Mismatches 34; Indels 1; Gaps 1;

Qy 1 EFPHHHHHTLSPSGPVTIIPPTVKLPHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60

Db 1 EFPHHHHHTLSPSGPVTIIPPTVKLPHSSCDPRGDAHSTIQLCLVSGFSPAKVHTW 60

Qy 61 LVDGGEAENLFPTTRKREGQTFSLOSEVNITQGMNSNTYTCYKHNGSIFEDSSR 120

Db 61 LVDGGEAENLFPTTRKREGQTFSLOSEVNITQGMNSNTYTCYKHNGSIFEDSSR 120

Qy 121 KCADSNPVGSAVLSPSPFDLIRKSPTITCLVVDLAPSKGTVNLTMRSASSKPVNHS 180

Db 121 RCSDPDEPRGVITYLPPSPIDVPLTCVLDI-ESEENITWYRERKSIGAS 179

Qy 181 RKEEKQNGTLYTSTLPGTRDWTIEGETYQCRVTHPHPLRALMRSTTKLPGRLAPEVY 240

Db 180 QRSTFHNNATTSITSLPUADKMEEGYQCRVDHPKPIVRSLKLPGRLAPEVY 239

241 MLPPSPETGTTRVTCIIRGYFPESEISQWLNFNEEDHTGHHTTRPQDHGHTDPSFL 300

Qy 301 YSRMLVNKSIWEKGNLVTCRVHEALPGSRTRLEKSLHYSGN 342

Db 300 YSRMLVNKSIWEKGNLVTCRVHEALPGSRTRLEKSLHYSGN 341

RESULT 11

US-10-673-594-3

Sequence 3, Application US/10673594

Publication No. US20040076625A1

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT APPLICATION NUMBER: US/10/673, 594

PRIOR APPLICATION NUMBER: 2003-09-29

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106, 652

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 3

LENGTH: 341

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically generated proteins
US-10-673-594-3

RESULT 13

US-10-176-6664-9

Sequence 9, Application US/10176664

Publication No. US20030031665A1

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT FILING DATE: 2002-06-19

PRIOR APPLICATION NUMBER: US/10/176,664

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Fast-SEQ for Windows Version 4.0

LENGTH: 341

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically Generated Proteins

US-10-176-6664-9

Query Match 84.5%; Score 1568.5; DB 14; Length 341;

Best Local Similarity 83.3%; Pred. No. 1.2e-116; Indels 1; Gaps 1;

Matches 285; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

Qy 1 EFPHHHHHTLSPESGPVTTIPPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTW 60

Db 1 EFPHHHHHTLSPESGPVTTIPPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTW 60

Qy 61 LVDCQEAEFLFPYTRPKREGQTFSLOSEVNTIQGWMSSNTYTCVKRNGSIFEDSSR 120

Db 61 LVDCQEAEFLFPYTRPKREGQTFSLOSEVNTIQGWMSSNTYTCVKRNGSIFEDSSR 120

Qy 121 KCADSNPGRGSAYLSRSPSPFDLFIKSPTITLVVDLAPSCKTVNLWSRASGPVNHST 180

Db 121 RCSDEPVGTVLIPPSPLDLYENGTPKLTLVLDI-ESENITYTVWRKKSIGSAS 179

Qy 181 RKSEKQRNGTLTVTSTLPVGTDRWIEGETYQCRVTHPLPRLMRSTTKLPGKRLAPEVY 240

Db 180 QRSTKHNNATTSISLPUFDADWIEEGYQCRVTDHFPIVRLTKLPGKRLAPEVY 239

RESULT 15

US-09-401-636-4

Sequence 4, Application US/09401636

Patent No. US2001008843A1

GENERAL INFORMATION:

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

FILE REFERENCE: 10223/006001

CURRENT FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: Fast-SEQ for Windows Version 4.0

SEQ ID NO 4

LENGTH: 341

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically Generated Proteins

US-09-401-636-4

Query Match 83.7%; Score 1553.5; DB 9; Length 341;

Best Local Similarity 82.7%; Pred. No. 1.9e-115; Indels 1; Gaps 1;

Matches 233; Conservative 21; Mismatches 37; Indels 1; Gaps 1;

Qy 1 EFPHHHHHTLSPESGPVTTIPPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTW 60

Db 1 EFPHHHHHTLSPESGPVTTIPPTVKLFHSSCDPRGDAHSTTQLCLVSGSPAKVHVTW 60

Qy 61 LVDCQEAEFLFPYTRPKREGQTFSLOSEVNTIQGWMSSNTYTCVKRNGSIFEDSSR 120

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Db      61 LVDGQEAEILFPYTRPREGGOTFSLOSEVNEITQGMSSNTYTCVKGNSIFEDSSR 120
Qy      121 KCADSNPRCVSAYLSRPSPFDLFIKRSPITITLUVVLDAPSXGTVNLTWSRASGKPYTHST 180
Db      121 RCSDEPRAVITYLIPSPDLDLENGTXLTCVLID-ESEENITYTVVRERKSGSAS 179
Qy      181 RKEEKQRNGLTIVTSTLPGTRDWIEGHTYOCRYTHPHLPRALMRSTTKLPGKRLAPEVY 240
Db      180 QRSKHHATTSTSILVDAKDWEGGYQCRVDHFPKPIVRSITKLPSKRLAPEVY 239
Db      241 MLPPSPETGTTTATYTCIRGFYPSEIYQWLENNEEDHTGHHTTRPQKDHGTDSPFL 300
Qy      240 MLPPSPETGTTTATYTCIRGFYPSEIYQWLENNEEDHTGHHTTRPQKDHGTDSPFL 299
Db      301 YSRMLVNGSIWEKGNLVICRVVHEALPOSRTLEKSUYSGN 342
Qy      300 YSRMLVNGSIWEKGNLVICRVVHEALPOSRTLEKSUYSGN 341
Db

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Search completed: November 14, 2004, 15:12:43
 Job time : 80 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 15:03:41 ; Search time 24 Seconds
(without alignments)
1371.089 Million cell updates/sec

Title: US-09-401-636-8
Perfect score: 1856
Sequence: 1 EFHHHHHTLSSLPPSGCPVTI.....HEALPGSRTLEKSLHYSGN 342

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1779556

Minimum DB seq length: 0
Maximum DB seq length: 342

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing First 45 summaries

Database : PIR 79;*

1: PIR1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	48.5	26.2	326	1 G2HU	Ig gamma-2 chain C
2	47.6	25.6	327	1 G4HU	Ig gamma-4 chain C
3	47.3	25.5	328	2 I47161	Ig gamma-3 chain C
4	46.8	25.2	328	2 I47160	Ig gamma-2b chain
5	46.5	25.1	328	2 I47159	Ig gamma-2a chain
6	46.3	25.0	328	2 I47158	Ig gamma-1 chain C
7	45.4	24.5	330	1 GHHU	Ig gamma-1 chain C
8	44.7	24.1	277	1 I47162	Ig gamma-4 chain C
9	43.5	23.9	322	2 PS0019	Ig gamma-2a chain
10	43.7	23.6	323	1 GHERB	Ig gamma chain C
11	43.6	23.5	326	1 PS0017	Ig gamma-1 chain C
12	42.8	23.1	329	2 S00847	Ig gamma-2c chain C
13	42.4	22.9	329	1 G2GP	Ig gamma-2 chain C
14	42.4	22.7	335	1 G2MSAB	Ig gamma-2a chain
15	41.8	22.5	308	2 C30554	Ig gamma heavy chain C
16	41.5	22.4	324	1 G1MS	Ig gamma-1 chain C
17	41.3	22.3	327	2 S06611	Ig gamma-2 chain C
18	40.2	21.7	255	4 S31866	Ig gamma-1 chain C
19	40.1	21.6	289	1 G3HUWI	Ig gamma-3 heavy C
20	39.7	21.4	329	1 G3MWS	Ig gamma-3 chain C
21	39.5	21.3	330	1 G2MSA	Ig gamma-2a chain
22	38.6	20.8	324	2 PT0207	Ig gamma chain C
23	38.4	20.7	333	2 PS0018	Ig gamma-2b chain
24	37.0	20.0	340	2 I56230	Ig alpha-2 chain C
25	36.9	19.9	340	1 A2HU	Ig alpha-2 chain C
26	35.9	19.4	340	1 A45966	Ig alpha chain C
27	34.3	18.5	342	2 A45966	Ig alpha chain C
28	31.8	17.2	342	2 I47175	Ig gamma heavy cha
29	30.8	16.6	180	2 I46732	

ALIGNMENTS

RESULT 1
G2HU
Ig gamma-2 chain C region - human
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1981 #sequence-revision 13-Jun-1983 #text_change 09-Jul-2004
C;Accession: A33906 ; A92809 ; A90752 ; A93132 ; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain co
A;Reference number: A93906 ; PMID:82197621 ; PMID:6804548
A;Molecule type: DNA
A;Accession: A33906
A;Residues: 1-326 <TLL>
A;Cross-references: UNIPROT:P01859 ; GB:V00554 ; GB:J00230 ; NID:932759 ; PIDN:CAB58438.1 ;
A;Note: Ly-326 is probably removed posttranslationally
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and
A;Content: number: A92809 ; PMID:81007873 ; PMID:6774012
A;Content: myeloma protein Trill
A;Accession: A3209
A;Molecule type: Protein
A;Residues: 1-197, Q1, 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A;Note: TRP-156 is at or near the complement-binding site
R;Connelly, G.B.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A;Title: The amino acid sequences of the three heavy chain constant region domains of a
A;Reference number: A90752 ; PMID:8001157 ; PMID:113060
A;Content: myeloma protein Zile
A;Accession: A30752
A;Molecule type: protein
A;Residues: 1-24, E, 26-57, 2Y, 60-85, 132-171, '222', 175, 'B', 177-193, 'D', 195-196, 'Q', 198
A;Note: this sequence has since been revised
R;Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 93-925, 1979
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin
A;Content: annotation; zie, revisions to residues 25, 59, 60, and 264-268
A;Reference number: A93132 ; PMID:80114419 ; PMID:118920
A;Content: zie
A;Accession: A93132
A;Molecule type: protein
A;Residues: 238-275 <HOF>
R;Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A;Reference number: A94591
A;Content: annotation; zie, revisions to residues 25, 59, 60, and 264-268
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
R;Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.
A;Reference number: A90253 ; PMID:194042
A;Content: annotation; myeloma protein Sa, disulfide bonds

QY 91 VNITQGOMSSNTTYCHVHNGSIFEDSSRK-----CADSNPFGVSAYLSPSPPF 140
 DB 69 VTPASS LSSKYYTCNVNHPATTTKDKVGTKTTPCP1CPGCVAQPVFIFPPPK 127
 QY 141 D-LFIRKSPITCLVVDLAPSQCTVNLTWSRASGKPYNHSTREKEKORNGTFLTVTSLTV 199
 DB 128 DTLYMSQPEVTCVVVDISKERAEVQFESWYDGVETHTAETRPKEQFNSTYRVSVLPI 187
 QY 200 GTRWIEGETYQCRVTHPHLPALMRSTTKLPKGKRLAPEVNMPLPSPEETGTR-TVYCL 258
 DB 188 QHQWLKGREFKCKVNNVDLPAPETRISKAQGSREQVYLPPAELRSKTVTVC 247
 QY 259 ICFYPSSETSVQWLNFNNEBEDGHTTRTPQDHGTPDSPEFLYSRMVLYNKSTWEKGNLVT 318
 DB 248 VIGYPPDIIHVKEVNSGNGEPEPGNYRTTPQQQ--VDTCTFFXSKLAVDKAWRDHBTFE 305
 QY 319 CRYTHEALPGSRTELEKSILHYSG 341
 DB 306 CAYNHEALHNHT-QKSISKTQG 327

RESULT 4
 147160 19 gamma 2b chain constant region - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C;Accession: 147160
 J;Immunol. 153, 3565-3573, 1994
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
 A;Reference number: 147158; MUID:95015845; PMID:7930579
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-328 <KAC>
 A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
 C;Genetics:
 A;Gene: IgG2b
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 F;133-202/Domain: immunoglobulin C region; immunoglobulin homology <IMM>

Query Match 25.1%; Score 465; DB 2; Length 328;
 Best Local Similarity 33.0%; Pred. No. 2.7e-27;
 Matches 111; Conservative 58; Mismatches 137; Indels 30; Gaps 10;

QY 22 PPTVLFHSSCDPDAHSTIQLLVLGSFSRPAKRVW---LVDGQEAENLFPYTRP 77
 DB 6 PSVYIAPCSRDTSG--PNVALGOLASSYFPEPVTVWNSGALS---VHTFPSVLQP 59
 QY 78 KREGGQTFSLQSEVNITQGOMSSNTYCHVHNGSIFEDSSRK-----CADSNP 127
 DB 60 ----SCLYSSMVTVPASS-LSSSYTVNHPATTKVDRVGTKXPDCIPACES 114
 QY 128 RGVSAYLSRSPSPFD-LFIRKSPITCLVVDLAPSQGTYNLTWSRASGKPYNHSTREKEQ 186
 DB 115 PGPSFIFPPKPKDQTMISRTPQTCVWVDSQEPYQFSWVTDGEVHTAQTRPKEEQ 174
 QY 187 RNTGTTVTSILPVGTRDMEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVNMPLPSPF 246
 DB 175 FNSTYRVSVSLPIQDWLNGKEPKCKVNNKDLPAPITRILISKAGQTREPQYTLPPHA 234
 QY 247 BETGGTR-TVTCIIGFYPEISVQWLNFNNEDEHTGHHTTRPOKDHDGTDPSFLYLSRML 305
 DB 235 BEILSSKVKSVTICLIVGTRDMEGETYQCRVTHPHLPALMRSTTKLPGRKLAPEVNMPLPSPF 292
 QY 306 VNKSWEKGNLVTCVHEALPGSRTLEKSILHYSG 341
 DB 293 VDKASWQGGGFQCAVMHEALHNHT-QXSISKTPG 327

RESULT 6
 147158 19 gamma 1 chain constant region - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C;Accession: 147158
 J;Immunol. 153, 3565-3573, 1994
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s
 A;Reference number: 147158; MUID:95015845; PMID:7930579
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-328 <KAC>
 A;Cross-references: EMBL:U03780; NID:9433125; PIDN:AAA52218.1; PID:9433126
 C;Genetics:
 A;Gene: IgG1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 F;133-202/Domain: immunoglobulin C region; immunoglobulin homology <IMM>

Query Match 25.0%; Score 463.5; DB 2; Length 328;
 Best Local Similarity 33.9%; Pred. No. 3.5e-27;
 Matches 107; Conservative 58; Mismatches 124; Indels 27; Gaps 9;

QY 42 IQLCIVSGSPAKRVW---LVDGQEAENLFPYTRPREGQQTFSLOQEYVINITGQ 97
 DB 147-59

23 VALGCLASSYFPPVPTWNSGALTSG--VHTFPSPVILQP---SGIYSLSMMTVPASS 75
 Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
 A;Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),
 igen Primärstruktur.
 A;Reference number: A91668; PMID:77070269;
 A;Contents: myeloma protein Nie
 A;Accession: B91668

A;Molecule type: protein
 A;Residues: 1-34 'Q' , 36-96 'K' , 98-115 'Q' , 117-197 'D' , 199-238 'D' , 240 'L' , 242-268 'E' , 27
 A;Note: This sequence has the Gim(17) and Gim(1) markers
 R;Schmidt, W.B.; Jung, H.D.; Palm, H.; Hilschmann, N.

135 TPEITCVVDVSKHAEYQFSWTDGVVEHTAETRPEKEQFRSTYRVSVLPIQHDWLK 194
 Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
 A;Title: Die Primärstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KOI
 A;Reference number: A91723; PMID:83289131; PMID:684994

147 SPTITCLVLDLASSKGITNLTWSRASERPKVNISTRKEBKORNGTLTISTLPVGTRDWIE 206
 A;Contents: myeloma protein KOI; disulfide bonds
 A;Accession: A91723

135 TPEITCVVDVSKHAEYQFSWTDGVVEHTAETRPEKEQFRSTYRVSVLPIQHDWLK 194
 A;Residues: 1-96 'R' , 98-197 'D' , 199-238 'E' , 240 'M' , 242-266 'D' , 268-271 'D' , 273-330 <SCH
 P;Gall, W.E.; Edelman, G.M.

195 GREFRCKVNNVNDPAPITRISAIGGSREPOVYTLPPAEELRSRKVTLCLVGFYPP 254
 Biochemistry 9, 3188-3196, 1970
 A;Contents: this sequence has the Gim(3) and Gim(non-1) markers
 A;Accession: A90565; PMID:71064027; PMID:4933144

196 EISQWLNNEEDHTGHHTTRPQKDGTDPSPFLYSRMLYNKSTMEKGHLVTCRVYHEA 325
 Hoppe-Seyler's Z. Physiol. Chem. 357, 155-1540, 1976
 A;Contents: annotation; disulfide bonds
 A;Reference number: A91667; PMID:77070267; PMID:1002129

255 DIIHFWKMGQPEPENTYTRTPPFQQD--VDGTFFLYSSKLAVIDKARWDHGDKPECAMHEA 312
 A;Contents: annotation; disulfide bonds
 A;Accession: A91667; PMID:77070267; PMID:1002129

326 LPSSRTLKLXSLHSAAG 341
 C;Species: Homo sapiens (man)
 C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
 C;Accession: A93433; S33686; S33687; B90563; A90564; B911668; A911723; A02146
 R;Ellison, J.W.; Berson, B.J.; Hood, L.E.
 Nucleic Acids Res. 10, 4071-4079, 1982
 A;Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
 A;Cross-references: UNIPROT:PO1857; EMBL:217370
 A;Accession: A93433; PMID:62874238;

19 gamma-1 chain C region - human
 A;Species: Homo sapiens (man)
 C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
 C;Accession: A93433; S33686; S33687; B90563; A90564; B911668; A911723; A02146
 R;Harris, L.J.
 Submitted to the EMBL Data Library, October 1992
 A;Reference number: S33684
 A;Accession: S33685
 A;Molecule type: DNA
 A;Residues: 1-330 <ELL>
 A;Cross-references: UNIPROT:PO1857; EMBL:217370
 A;Accession: A93433
 A;Cross-references: EMBL:217370
 A;Accession: B90563
 A;Molecule type: DNA
 A;Residues: 2-330 <ELL>
 A;Cross-references: EMBL:217370
 Cell 29, 671-679, 1982
 A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
 A;Reference number: S33687; PMID:83001943;
 A;Accession: S33687
 A;Molecule type: DNA
 A;Residues: 1-113; 235-330 <TAK>
 A;Cross-references: EMBL:217370
 R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
 Biochemistry 9, 3161-3170, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
 A;Reference number: A90563; PMID:71064024; PMID:5489771
 A;Contents: myeloma protein Eu
 A;Accession: B90563
 A;Molecule type: protein
 A;Residues: 1-96 'R' , 98-135 <CIN>
 A;Note: this sequence has the Gim(3) marker, 97-ArG
 R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
 A;Reference number: A90564; PMID:71064025; PMID:5530842
 A;Contents: Eu
 A;Accession: A90564
 A;Molecule type: protein
 A;Residues: 136-154, 'Q' , 156-165, 'Q' , 167-176, 'Q' , 178-194, 'N' , 196-197, 'D' , 199-238, 'E' , 240,
 A;Note: this sequence has the Gim(non-1) markers, 239-Glu and 241-Met
 R;Ponstingl, H.; Hilschmann, N.

RESULT 7
 GHNU
 19 gamma-1 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004
 C;Accession: A93433; S33686; S33687; B90563; A90564; B911668; A911723; A02146
 R;Harris, L.J.
 Submitted to the EMBL Data Library, October 1992
 A;Reference number: S33684
 A;Accession: S33685
 A;Molecule type: DNA
 A;Residues: 1-330 <ELL>
 A;Cross-references: UNIPROT:PO1857; EMBL:217370
 A;Accession: A93433
 A;Cross-references: EMBL:217370
 A;Accession: B90563
 A;Molecule type: DNA
 A;Residues: 2-330 <ELL>
 A;Cross-references: EMBL:217370
 Cell 29, 671-679, 1982
 A;Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
 A;Reference number: S33687; PMID:83001943;
 A;Accession: S33687
 A;Molecule type: DNA
 A;Residues: 1-113; 235-330 <TAK>
 A;Cross-references: EMBL:217370
 R;Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman,
 Biochemistry 9, 3161-3170, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen
 A;Reference number: A90563; PMID:71064024; PMID:5489771
 A;Contents: myeloma protein Eu
 A;Accession: B90563
 A;Molecule type: protein
 A;Residues: 1-96 'R' , 98-135 <CIN>
 A;Note: this sequence has the Gim(3) marker, 97-ArG
 R;Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
 Biochemistry 9, 3171-3181, 1970
 A;Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequen
 A;Reference number: A90564; PMID:71064025; PMID:5530842
 A;Contents: Eu
 A;Accession: A90564
 A;Molecule type: protein
 A;Residues: 136-154, 'Q' , 156-165, 'Q' , 167-176, 'Q' , 178-194, 'N' , 196-197, 'D' , 199-238, 'E' , 240,
 A;Note: this sequence has the Gim(non-1) markers, 239-Glu and 241-Met
 R;Ponstingl, H.; Hilschmann, N.

Query Match 24.5% Score 454; DB 1; Length 330;
 Best Local Similarity 34.4%; Pred. No. 1; 8e-16;
 Matches 117; Conservative 57; Mismatches 130; Indels 36; Gaps 12;

22 PPTVKLFISSCDPRGDASHIOTLCLVSGPSAKVHYTW---LVDCQEAENLFPYPTTRP 77
 QY 6 PSVYPLAPS SKSTSG---GTAALGCLVKDIFPPPTVSNSCALTSQ---VHTFPAVL-- 57

78 KREGGGQTFSLQSSEVNTIQGMNSNTTCHVYHNGSIFE-----DSSRKC---A 123
 DB 58 --QESGLYSLSSSYTVPSSS-LGTCQTMVNYHKSPTKIVDKRVEPKSDKTHTCPCPA 114

124 DSNPRGVSAYLSRSPSPFD-LFIRKSPITLCLVYDLSRKGTVNLTSRASGKPVNHSRK 182
 DB 115 PELLGGPSVFLFPKPKDTLMISRPTVTCVVYDVSHEDPEVKENVYDGVYEVRAKTKP 174

183 EFKQRNGLTVTSTLPVGRDWEGETYQCRVTHPHLPRALMSTKLPGKRLAPPVYML 242
 QY 175 REEDYNSTYRVSVLTIHQDNNGKEYKCVNSKALPAPELKTSKAGQPREPVYLT 234

DB 174 PPSPEE-TGTTRTVTCIJRGFVPSSEIVSQWLNEEDHTGHTRPQDHDGTDPSFFLY 301
 QY 293 SRLMLVNSKIWEKGNLVTCRVWEHALPGRSLTEKSLHYSG 341

DB 235 PPSRDELTKNQSLTCLVYKGFPSD-AVEWSNGQEN- NYKTFPPVLD--SDGSSFYLY 290

302 SRLMLVNSKIWEKGNLVTCRVWEHALPGRSLTEKSLHYSG 341

DB 291 SKLTVDSRWRQQNVPSCSVMHEALNHYT-QKSLSLSPG 329

RESULT 8
 147162 Ig Gamma-4 chain constant region - pig (fragment)
 C;Species: Sus scrofa domestica (domestic Pig)
 C;Accession: I47162 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 R;Fracskovic, I.; Sun, J.; Butler, J.E.
 J;Immuno: 15.; 3565-3573, 1994
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a set of 82-151/Domain: immunoglobulin homology <IMM>
 A;Accession: I47162
 A;Status: Preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-277 <KAC>
 A;Cross-references: EMBL:U03782; NID:9433129; PID:9433130
 C;Gene: IgG4
 C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
 F;82-151/Domain: immunoglobulin homology <IMM>

Query Match 23.9%; Score 443.5; DB 2; Length 322;
 Best Local Similarity 34.4%; Pred. No. 1..1e-25;
 Matches 110; Conservative 50; Mismatches 127; Indels 33; Gaps 12;

Qy 38 AHSTIQOLLCLIVSGRSPAKHVTW---LYDQGQEABNLFPYTRPREGGQTFSLSQSEVNI 93
 Db 19 SNSVTLGCLVKGYPPEPVTVTANSALSSG---WHTPAVLQ---SGLYLTTSVTV 70

Qy 94 TQGOMISSNTYTCYTHNGSIFEDSS---RKCADSNPRGV----SAYLRSRSPSPFD_L 142
 Db 71 PSSTW-SSQAVTCNAHPASSTKDKVTPREC---NPGCCTGSVESSVFIFPPKTKDVL 126

Qy 143 FIRKSPITCLVVDLAPSKGTVNLTWSRASGKPVNTHSTRKEEKGNGTLTVTSPVGR 202
 Db 127 TITLPBKVTCVVNDISQNDEPVRSWFIDDOVEHTAQTAPHAPEXNSNTRSVSPLPIVER 186

Qy 203 DWIEGETYQCRVTHPHPLRALMRSTKLPGKRLAPEVY ML2PSPEETGTTTIVTCLRG 261
 Db 187 DWINGTFKCKVNSGAFAPIERKSISKEPGETPRQPVYTMAPPREMTQSQVSITCMYKG 246

Qy 262 FYPSETSVQWLFNNEDHTGHHTTRPQDHGTDSFLFLYSRMLVINKSIEWGNLVTCRV 321
 Db 247 FYPDPDTYEMKMGDQE--NYKNTTPPTMD--TGGSYFLYSKLNVKETWQQGNTFTCSV 302

Qy 322 VHEAPFGSRTEKSHRYHSAG 341
 Db 303 LHEGLHNHT-EKSISHSPG 321

RESULT 10
 Ig gamma chain C region - rabbit
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 24-Apr-1994 #sequence 15-Nov-1981
 C;Accession: A91749; A90290; A93928; A90245; A94416; A02161
 R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.
 Immunogenetics 18, 307-329, 1983
 A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplo
 A;Reference number: A91749; MUID:84030330; PMID:6313520
 A;Accession: A91749
 A;Molecule type: mRNA
 A;Residues: 1-323 <BER>
 A;Cross-references: UNIPROT:F01870
 A;Note: this sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Th
 A;Molecule type: protein
 R;Pratt, D.M.; Mole, L.E.
 Biochem. J. 151, 317-349, 1975
 A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglo
 A;Accession: A90290
 A;Molecule type: protein
 R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
 A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chai
 A;Reference number: A93928; MUID:83299917; PMID:6193512
 A;Accession: A93928
 A;Molecule type: mRNA
 A;Residues: 88-103 'M', '105-143', 'E', '145-184', 'A', '186', 'E', '188-266 <MAR>
 A;Cross-references: GB:M16426; NID:915111; P10N:AAA312891; PID:GI65112
 A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic mark
 R;Frucht, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
 Biochem. J. 116, 249-259, 1970
 A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
 A;Reference number: A90245
 A;Accession: A90245
 A;Molecule type: protein
 A;Residues: 122-143, 'E', '145-161 <FRU>
 R;Hill, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
 In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127. Almquist and Wiksell
 A;Reference number: A94416
 A;Accession: A94416

RESULT 9
 19 Gamma-2a chain C region - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 R;Brueggemann, M.
 Gene 74, 473-482, 1988
 A;Title: Evolution of the rat immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
 A;Reference number: PS0017; MUID:89232738; PMID:3149946
 A;Accession: PS0019
 A;Molecule type: DNA
 A;Residues: 1-322 <BRU>
 A;Cross-references: UNIPROT:P20760
 R;Brueggemann, M.; Freis, J.; Diamond, A.; Howard, J.; Cobbola, S.; Waldmann, H.
 Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
 A;Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
 A;Reference number: D25941
 A;Accession: D25941
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 216-322 <BR2>
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin

A: Molecule type: protein
 A: Residues: 129-131:155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-222,'Q'
 A: Note: this has the e15 allotypic marker, 185-Ala
 C: Complex: An immunoglobulin heterotrimer subunit consists of two identical light (Kappa) chains disulfid bonded. In some cases, such as IgA and IgM, the subunits associate into larger complexes.
 C: Superfamily: immunoglobulin C region; immunoglobulin homology
 C: Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin; immunoglobulin P; 20-82:Domain: immunoglobulin homology <IM1>
 F; 1-26-303/Domain: immunoglobulin homology <IM3>
 F; 173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match Score 437.5%; DB 1; Length 323;
 Best Local Similarity 34.3%; Pred. No. 2.9e-25;
 Matches 113; Conservative 61; Mismatches 110; Indels 45; Gaps 14;

Qy 36 GDA-HSTIQLCLVSGFSPAKVHVTW---LVDGQEAENLFPYTRPKREGQTFSLQE 90
 Db 16 GDPSSVTTGKLVGVLQPEPVTVNSGTLTNGVET--PPSV--ROSSGLYSSLSSV 68

Qy 91 VNTTCQKMSNTYTCVHKH-----NGSIFEDSSRKCADSNPR--GVSAYLSRSPSPF 140
 Db 69 VSVTIS----SSQFVTCNVAVHPATNTKVDTKVAPOSTCSKPTOPPPELGGSVFIPPKER 124

Qy 141 D-LFIRKSPTICLVNDLAPSKGTVNLW----SRASGKPVNHSTRKEKOINGTLVY 193
 Db 125 DTLMISRSPTEVTCVWWBVSQDDEPEQFTWYINNEQRTARPL----REQQFESTIV 178

Qy 194 TSTLPVGTRDWIEGETVQCRVTHPHIPRAAMRSTKLPGKRLAPEVY-MIPLPSPREGT 252
 Db 179 VSTLPITHQDLRGKEFKCKVHNKAPEKTIKARQGLEPKVYTMCPREELSSRS 238

Qy 253 RTVTLCLRGYPSEISVQWLFWNNEDEHTGHHTTRPKQDHTDTPSFPELYKMLNKSVIE 312
 Db 239 VSTLCMIGYPSEISVQWLFWNNEDEHTGHHTTRPKQDHTDTPSFPELYKMLNKSVIE 294

Qy 313 KGNLVTCRVHEALPGSRTLEKXLSLHYSAQ 341
 Db 295 RGDVFTCSVMEALHNHYT-QKSISRSRSPG 322

RESULT 11
 PS0017 IS Gamma-1 chain C region - rat
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004
 C:Accession: PS0017; C25941;
 R:Brueggemann, M.
 Gene: 74, 73-482, 1988
 A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
 A:Reference number: PS0017; MUID:89232736; PMID:3149946
 A:Accession: PS0017
 A:Residues: 1-326

 A:Superfamily: UNIPROT:P20759
 A:Keywords: immunoglobulin heavy chain locus of the rat; striking homology to mouse antibody
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 220-326

 C:Genetics:
 A:Introns: 98/1; 113/1; 220/1
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin P; 20-84:Domain: immunoglobulin homology <IM>

Query Match Score 23.5%; DB 2; Length 356;
 Best Local Similarity 32.7%; Pred. No. 3.5e-55;
 Matches 105; Conservative 54; Mismatches 131; Indels 31; Gaps 10;

Qy 38 AHSTIQLCLVSGFSPAKVHVTW---LVDGQEAENLFPYTRPKREGQTFSLQE 93
 Db 19 SNSMTVTLGCLVKGYPFPVPTVNSGALSSG---VHTPAVLQ---SGLYLTTSVTV 70

Qy 94 TQGQWMSNTYTCVHKH-----NGSIFEDSSRKCADSNPRGVSAYLSRSPFD-
 Db 71 PSSSW-PFQTYCVCNAVPASSTRKVDKIVPRNCGGDKRPCCTGSEVVSSVIFPPXPKD 129

Qy 142 L-FIRKSPTICLVNDLAPSKGTVNLW-SRASGKPVNHSTRKEKOINGTLVY-TPLVGT 201
 Db 130 LTTLTLPKTVVWDIQDDPFVHFSEVDFEVHTAQTRPPEEQNSTRFSVSELPLH 189

Qy 202 RDWIEGETVQCRVTHPHIPRAAMRSTKLPGKRLAPEVYMLPPSPBE-TGTRTRVTCILR 260
 Db 190 QDWNINGRTRFRCKVTSAAFPSPIEKTLISKPEERTQVPHVYTMSPTEKMTNEVSITCMVK 249

Qy 261 GFYPSEISVQWLFWNNEDEHTGHHTTRPKQDHTDTPSFPELYKMLNKSVIE 320
 Db 250 GFYPDPDVYEWQMNGQOE- NYKNTFPTMD-TDSSGFYLSKLNKVKERKQGNTFTCS 305

Qy 321 VVHEALPGSRTLEKXLSLHYSAQ 341
 Db 306 VLIHGLHNHHT-EKSLSHSRSPG 325

RESULT 12
 S00147
 19 Gamma-2c chain C region - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Sequence_revision 01-Dec-1989 #text_change 09-Jul-2004
 C:Accession: S00147
 R:Brueggemann, M.; Delmastro-Galfre, P.; Waldmann, H.; Calabi, F.
 Eur. J. Immunol. 18, 317-319, 1988
 A:Title: Sequence of a rat immunoglobulin gamma-2c heavy chain constant region cDNA: ext
 A:Reference number: S00147; MUID:88166903; PMID:3127222
 A:Accession: S00147
 A:Molecule type: mRNA
 A:Residues: 1-329

 A:Cross references: UNIPROT:P20762; EMBL:X07189; NID:977602; PID:CAA30169.1; PMID:966322
 C:Supertertiary: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin
 F; 20-84/Domain: immunoglobulin homology <IM>

Query Match Score 23.1%; DB 2; Length 329;
 Best Local Similarity 32.4%; Pred. No. 1.5e-20;
 Matches 110; Mismatches 59; Indels 36; Gaps 13;

Qy 23 PTYKLFHSSCDPGRDAHSTIQCLVSGFSPKAVHVTW---LVDGCEAENLFPYTRPK 78
 Db 6 PSVPLVPGCS-GTGSALVTVGCLVGYFPPBVTKWNSGALSSG--VHTFPAVLQ-- 58

Qy 79 REGQFISLQSEYNTIQGOMMSNTYTCVHKH---NGSIFEDSSRK-
 Db 59 ---SGLYLTSSVTPVSSWT-SQSTVTCVSAHPATNSNLKRIEPPKPRPTDICS 114

Qy 125 SNPLGRPSVIFPPKPKDILMITLPKTVCVYDVSBEPDQFSWVPTDNRVFTAQPH 183
 Db 115 EQLNGTFRVVKNNKDLPSPIEKTKISPRGKARTPQVTTIP 234

Qy 164 EKQNGLITVSTLPVGTRDWIEGETVQCRVTHPHIPRAAMRSTKLPGKRLAPEVYMLP 243
 Db 175 EQLNGTFRVVKNNKDLPSPIEKTKISPRGKARTPQVTTIP 234

Qy 244 PSPBEGTGTTR-TVTCILRGFYSEISVQWLFWNNEDEHTGHHTTRPKDHTDTPSFLYS 302
 Db 235 PPREQMSRKNSVTSFVYASISWEVNGELQ-DYKNTLFLVLD--SDESFLYS 290

Qy 303 RMVLNKSWEKGNLVTCRVVHEALPNHHT-QKNLRSRSPG 341
 Db 291 KLSVYDTSWMRGDIYTCSVHEALHNHT-QKNLRSRSPG 328

RESULT 13

G2GP Ig Gamma-2 chain C region - guinea pig C;Species: Cavia porcellus (guinea pig) C;Date: 07-May-1981 #sequence revision 07-May-1981 #text change 09-Jul-2004 C;Accession: A94553; A90352; A90359; A90384; A90385; A02151 R;Trischmann, T.M. submitted to the Atlas, April 1975 A;Reference number: A94553 A;Accession: A94553 A;Molecule type: protein A;Residues: 1-3 <TR1> A;Cross-references: UNIPROT: P01862 R;Birshaini, B.K.; Hussain, Q.Z.; Cebray, J.J. Biochemistry 10, 9-17, 1971 A;Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Am A;Reference number: A90359; MUID:5538616 A;Accession: A90359 A;Molecule type: protein A;Residues: 69-133.12-29 <TUR> R;Trachem, D.B.; Cebray, J.J. Biochemistry 13, 4796-4803, 1974 A;Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies. A;Reference number: A90384; MUID:75036072; PMID:4429665 A;Accession: A90384 A;Molecule type: protein A;Residues: 134-226 <TRA> R;Trischmann, T.M.; Cebray, J.J. Biochemistry 13, 4804-4811, 1974 A;Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies. A;Reference number: A90385; MUID:75036073; PMID:4603467 A;Accession: A90385 A;Molecule type: protein A;Residues: 227-311 <TR2> R;Oliveira, B.; Lamm, M.E. Biochemistry 10, 26-31, 1971 A;Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin. A;Contents: annotation: disulfide bonds A;Note: Cys-16 is involved in a heavy-light chain bond C;Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs. C;Complex: An immunoglobulin heterotrimer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin F:21-81/Domain: immunoglobulin homology <IM1> F:135-204/Domain: immunoglobulin homology <IM2> F:241-310/Domain: immunoglobulin homology <IM3> F:142-202/Disulfide bonds: #status experimental F:178/Binding site: carbohydrate (Asn) (covalent) #status predicted F:248-308/Disulfide bonds: #status experimental	Db 108 PRCPPENLGGGSVTFPPKCDTDMTSLPRVTVQFVWFSQDEPVQFVWFSVQKPVG 166 Qy 177 NHSTRKKEKQNGNTLVTTSLPVGTRDWEGETYQCRVTHPHPLRMLRSITKLPGRLA 236 Db 167 NAETKPKVEQNTTFRVESVLPIQHQDWIRKEKCVKVNKAALPAIEKTIKSKTGAPRM 226 Qy 237 PEVYMLPSPSEPTGTR-TVTLGLRGYPSETSVQWLNFNEBEDHTGHHTTRPQKDGTG 295 Db 227 PDYTLPPSRDLSKSKVSTCLTINFPADIHVEMASNRPVSSKEYKNTTPPIED-AD 284 Qy 296 PSFFLYSRLYNKSIWEGNLUVTCRVHEALPGSRTLEKSLHYSG 341 Db 285 GSYFLISKLTVDKSANDQGTVTCSYMEHALHNHVT-QKAISSPG 329
RESULT 14	
G2MSAB Ig Gamma-2a chain C region, secreted form (allele b) - mouse C;Species: Mus musculus (house mouse) C;Date: 02-Apr-1982 #sequence revision 02-Apr-1982 #text_change 09-Jul-2004 R;Dogmin, M.J.; Lawrence, M.; Strosberg, A.D. Proc. Natl. Acad. Sci. U.S.A., 78, 4031-4035, 1981. A;Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc region A;Reference number: A02153; MUID:6170055; PMID:6170055 A;Accession: A02153 A;Molecule type: mRNA A;Residues: 1-35 <SCH> A;Cross-references: UNIPROT: P01864; GB-J00479 A;Experimental source: strain C57Bl/6 R;Dogmin, M.J.; Lawrence, M.; Strosberg, A.D. Proc. Natl. Acad. Sci. U.S.A., 78, 4031-4035, 1981. A;Title: Multiple amino acid substitutions between murine gamma 2a heavy chain Fc region A;Reference number: A32656; MUID:82037777; PMID:6794027 A;Accession: A32656 A;Molecule type: protein A;Residues: 118-267, E-269-328, 'G-330-334 <DOG> C;Comment: Lys-335 is removed posttranslationally. C;Complex: The sequence differs from that of the allele from BALB/C mice, at 15% of chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C;Superfamily: immunoglobulin C region; immunoglobulin homology C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F:98-118/Region: hinge P:142-211/Domain: immunoglobulin homology <IM2> P:148-315/Domain: immunoglobulin homology <IM3> P:155/Disulfide bonds: interchain (to light chain) #status predicted P:27-82, 149-209, 255-313/Disulfide bonds: #status predicted P:108,-11/Disulfide bonds: interchain (to heavy chain) #status predicted P:185/Binding site: carbohydrate (Asn) (covalent) #status predicted F:98-118/Region: hinge P:142-211/Domain: immunoglobulin homology <IM2> P:148-315/Domain: immunoglobulin homology <IM3> P:155/Disulfide bonds: interchain (to light chain) #status predicted P:27-82, 149-209, 255-313/Disulfide bonds: #status predicted P:108,-11/Disulfide bonds: interchain (to heavy chain) #status predicted P:185/Binding site: carbohydrate (Asn) (covalent) #status predicted	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;
Qy 36 GDAHHTIQLICLVSFSPAKVHTW---LVDGQEAENLFPTYTRKREGGQTFSLQSEV 91 Db 17 GTTGSSVTLGGLVKGYFPEPVLTWNSGLSSGVH-----TPALLQSGLYTLSSV 68	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;
Qy 92 NITQQWMSNTYTCHVKGNSLFEDSSRKCADSNPR----- Db 69 TVTSNTW-PSQTITCNVAHPAS---STRVDKKLEPRVPTQNCPHQRVPDCAPPIL 128	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;
Qy 129 -GVSAYLRSRSPFD-LFEKSPFTLCLVYDAPSKGTYNLTRSSGKPVNHSSTREEKQ 186 Db 124 GGPSFIFPPKIKDVLMLSSLSPMVTCVWVDSDDPDYQISWFVNVEVHTAQOTHRED 183	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;
Qy 187 RNCIITVTTSLPVGTRDWEGETYQCRVTHPHPLRMLRSITKLPGRLAEPVYMLPPSP 246 Db 184 YNSTLRRVSVSALP1QHDNMSGRFKCKVNRAPLSPTEKTISKPRGVPVRAQVYVLPFFPA 243	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;
Qy 19 TIPPTVKEFHSSCDPDDAHTIQLLVSGSPARVHW---LVDGQEAENLFPTY 74 Db 4 TTAPSVPPLAAASCYDTSG--SMMTLGGLVKGYFPEPVTVKNSGALTSG--VHTFPAV 57	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;
Qy 75 TRKREGGQTFSLOSEVNTQGMNSNTYTCHVKGNSLFIDDSSR----- 120 Db 58 LQ----SGLYVTSNTMVP---SSQKATONVAFASPSVDPK 107	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;
Qy 121 -XCSMSPRGYSAYLSPSPSPFD-LFIRKSPPITCLVYDAPSKGTVNLMSRASGKPV- 176	Query Match 22.7%; Score 421; DB 1; Length 335; Best Local Similarity 31.7%; Pred. No. 5.2e-24; Matches 106; Conservative 54; Mismatches 124; Indels 50; Gaps 9;

Qy 247 EE-TGTTRTVTCILRGFPESELQWLNNEEDHTGHHTTTRPQDKDHTGTPSPFLYSLRML 305
 Db 244 EENTKGEFSLTMITGFLPAEAVDTTSNGTEQNYKNTATVLD---SDGSYFMYSKLR 299.

Qy 306 VNKSIWEKGNLTYCIVTHEALPG--SRTLEKSL 336
 Db 300 YOKSTWERGSLPACSVYHEVANHLLTAKTISRSKL 333

RESULT 15

C30554 Ig heavy chain C region - sheep (fragment)

C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C;Date: 03-Mar-1989 #sequence_revision 03-Mar-1989 #text_change 21-Jan-2000

C;Accession: C30554

R;Foley, R.C.; Beh, K.J.

J. Immunol. 142: 708-711, 1989

A;Title: Isolation and sequence of sheep Ig H and L chain cDNA.

A;Reference number: A30554; PMID:2492052

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-308 <FOL>

C;Superfamily: immunoglobulin C region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;113-182/Domain: immunoglobulin homology < IMM>

Query Match 22.5%; Score 418; DB 2; Length 308;
 Best Local Similarity 33.3%; Prd. No. 7.9e-24;
 Matches 106; Conservative 54; Mismatches 122; Indels 36; Gaps 11;Qy 46 CLVSGFSPARKVWTW---LIVSQEARNLFPYITTRPKRECCOTPSLOSEVNII--TQGW 98
 Db 4 CLVSYMPPEVTWNNSGALTSG--WHTFPAIL---QSSLYSSSVTVPASTSG-- 54Qy 99 MSSNTYTCVKRNGSIFBDSSR--KCAD-----SNPRGVSAYLESPSPFD-LFI 144
 Db 55 --AGTPICVAHASSRKYRVEPGCPDPCKHCRCPPELPGGPVFIFPPKPKDRLI 112Qy 145 RKSPNITCVUVDLAPSKCENVNLITWSRASGKPVHSTREREKONGLTIVTSTLPVGTRDW 204
 Db 113 SGTEBEVTCVVDVGQDDPPEVQSMFVDNVEVRTARTPREEENSIFRVNSALPIQHODN 172Qy 205 IEGTYQCRTHPHPLRALMRSTTKLPGKRLAPEVYML-PPPEETGTTRTVTCLIRGFY 263
 Db 173 TGGGEFKCVAHVNEALPAPPVRTISRTKQAREPQVYLLAPPDEELSKSTLSYTCLVTFY 232Qy 264 PSEISVONLFNNNEEDHTGHHTTTRPQDKDHTGTPSPFLYSLRMLVNUKSISWERGENLVTCRVVH 323
 Db 233 PDYTAEVENQKNGQBESEDYGTTSQOLD--ADCSYFLSRDVQNSWQEGTYACVVMH 290

Qy 324 BALPSRTRLEKSLHYSG 341

Db 291 EALFHNYT-QKSISKPPG 307

Search completed: November 14, 2004, 15:07:21

Job time : 25 secs

Result No.	Score	Query Match	Length	DB ID	Description
1	486.5	26.2	326	1 GC2_HUMAN	P01859 homo sapien
2	428.5	26.0	337	2 Q95m34	Q95m34 equus caballus
3	476	25.6	327	1 QC4_HUMAN	P01861 homo sapien
4	454	24.5	330	1 GCI_HUMAN	P01857 homo sapien
5	433.5	23.9	322	1 GCA_RAT	P01870 ratmus norvegicus
6	437.5	23.6	323	1 GCI_RABIT	P02075 oryctolagus cuniculus
7	436.5	23.5	326	1 GCC_RAT	P20762 rattus norvegicus
8	424.8	23.1	329	1 GC2_CAVPO	P01862 cavia porcellus
9	424.5	22.9	329	1 GCAB_MOUSE	P01864 mus musculus
10	414.21	22.7	335	1 GCI_MOUSE	P01868 mus musculus
11	415.5	22.4	324	1 GCI_HOUSE	P01860 homo sapien
12	401.5	21.6	290	1 GC3_HUMAN	P01866 mus musculus
13	399.5	21.5	336	1 GCB_MOUSE	P22436 mus musculus
14	397	21.4	329	1 GCA_MOUSE	P01863 mus musculus
15	395.5	21.3	330	1 GCAA_MOUSE	P20761 rattus norvegicus
16	384	20.7	333	1 GCB_RAT	P01877 homo sapien
17	369.5	22.4	340	1 ALC2_HUMAN	Q6Kam2 mus musculus
18	334.5	18.0	303	2 Q6Ran2	Bad21135 mus musculus
19	334.5	18.0	303	2 BAD1435	P01879 oryctolagus cuniculus
20	260	14.0	299	1 ALC_RABIT	Badd0198 camelus dromedarius
21	228	12.3	169	2 BAD0198	Badd0199 camelus dromedarius
22	224	12.1	190	2 BAD0199	Badd0197 camelus dromedarius
23	177.5	9.6	156	2 BADD0197	Aah30813 homo sapien
24	171.6	9.5	234	2 AAH30813	Bac85234 homo sapien
25	173.5	9.3	240	2 Q6PHT5	Q6PHT5 homo sapien
26	173	9.3	236	2 Q6GNX9	Q6GNX9 homo sapien
27	173	9.3	236	2 AAH63199	Aah29444 homo sapien
28	173	9.3	236	2 AAH29444	O90524 ginglymostoma gallus gallus
29	167.5	9.0	268	2 Q90524	Q6PHT7 homo sapien
30	166.5	9.0	236	2 AAH34141	Aah34141 homo sapien
31	166.5	9.0	236		

RA Hofmann T., Parr D.M.; "A note of the amino acid sequence of residues 381-391 of human immunoglobulins gamma chains"; Mol. Immunol. 16:923-925(1979).
 RT MOL. IMMUNOL. 16:923-925(1979).
 RL [7]
 RN 25; 59; 60 AND 264-268 (ZIE).
 RA Hofmann T., Parr D.M.; Submitted (MAR-1980) to the PIR data bank.
 RL [8]
 SEQUENCE OF 1-121 (DOR).
 MEDLINE 95255298; PubMed=7737190;
 RA Scoppiati M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.; "Characterization of the two unique human anti-flavin monoclonal immunoglobulins." / Eur. J. Biochem. 228:886-893(1995).
 RN [9]
 RP DISULFIDE BONDS.
 RP DISULFIDE BONDS.
 RA Milstein C., Frangione B.; "Disulphide bridges of the heavy chain of human immunoglobulin G2." / Biochem. J. 121:217-225(1971).
 RN [10]
 RP DISULFIDE BONDS.
 RX MEDLINE 69064124; PubMed=5782707;
 RA Frangione B., Milstein C., Pink J.R.L.; "Structural studies of immunoglobulin G." / Nature 221:145-148(1969).
 RL [11]

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 CC EMBL; J00230; PAB59393.1; -.
 DR HSSP; P01857; 100%;
 DR Genew; FGNC; 5526; IGHG2.
 DR MIM; 147110; -.
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F: antigen binding; TAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig_C1.
 DR SMART; SM00407; IgC1_2.
 DR PROSITE; PS50835; Ig_LIKE; 3.
 DR PROSITE; PS00290; Ig_MHC; 2.
 KW Direct protein sequencing; immunoglobulin C region; Immunoglobulin domain.
 FT NON_TER 1 1
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 1 99 Hinge.
 FT DOMAIN 1 110 CH2.
 FT DOMAIN 111 219 CH2.
 FT DOMAIN 220 326 CH3.
 FT DISULFID 14 14 Interchain (with a light chain).
 FT DISULFID 27 83 Interchain (with a heavy chain).
 FT DISULFID 102 102 Interchain (with a heavy chain).
 FT DISULFID 103 103 Interchain (with a heavy chain).
 FT DISULFID 106 106 Interchain (with a heavy chain).
 FT DISULFID 109 109 Interchain (with a heavy chain).
 FT DISULFID 140 200 Interchain (with a heavy chain).
 FT DISULFID 246 304 AT OR NEAR THE COMPLEMENT-BINDING SITE.
 FT SITE 156 156 S -> A (in myeloma proteins T1L and ZIE).
 FT VARIANT 60 60 Query Match

Best Local Similarity 36.2%; Pred. No. 2.4e-29; Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11; QY 35 RGDAHSTQQLCLIVSGFSPAKVHVTW---LYDGQEAENLFPTPKREGQTSPLQSE 90
 DB 16 RSTSESTAALGCLVKDVFPEPVTSNSMIGALTSG--VHTFPAVL--QSSGLYLSVV 68
 QY 91 VNITQGOMSSNTTCYAVTH--NGSFDERSKCADSNP-----RGVAYLSPSPF 140
 DB 69 VTVYSSNF-GTQYTCNDHK-SNTKVDTKVERKCVCECPGAPPAGPSVFLFPKPK 127
 QY 141 D-LPIRKSPPTICLVVVDLAPSKGTQVNLTWSRASGKPVNHSTRKEEKGNGTLTVTSTLPV 199
 DB 128 DTLMISRTPEVTTVWVYSHEDDEVQNWNYDGVVNAKTKPRECFNSTFRVSVLTV 187
 QY 200 GTRDWIGETTYQCRVTHPHPLPMLRSSTKLPGKRLAPEVYMLPPSPPE-TGTTTVC 258
 DB 168 VHDDWLNGKEYKCKVSNGLPAPIEKTSKUQGPQVYLPPREBEMTMKNQVSLTCL 247
 QY 259 IRGYPPSEISVQWLFNNEQDHTTRQRDHGTPDPSFLYSRMVNLVNIWEKVLV 318
 DB 248 VKGFYPSPSDIAVEMBSNGOPEN--NYKTFPPMLD--SGSGSPFLYSKLTVDKSRWQOCNVS 303
 QY 319 CRVYHEALPGSRTLEKSILHYSG 341
 DB 304 CSVYHEALHNHY-QKSLSLSPG 325

RESULT 2
 Q95M34 PRELIMINARY; PRT; 337 AA.
 ID Q95M34
 AC Q95M34
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-MAR-2004 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DB Immunoglobulin gamma 1 heavy chain constant region (Fragment).
 Name:IGG1;
 GN Equus_caballus (Horse).
 CS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 NCBI_TaxID=9776;
 RN [1] _
 RN SEQUENCE FROM N.A.
 RX MEDLINE=8383416; PubMed=9717671;
 RA Wagner B., Overesch G., Sheoran A., Holmes M., Richards C., Leibold W., Radbruch A.,
 RT "Organization of the six horse IgH Genes and corresponding ImmunoGenetics 54:1353-1364 (2002).
 RL ImmunoGenetics 199:105-118 (1998).
 RN [2] _
 RN SEQUENCE FROM N.A.
 RX MEDLINE=22172648; PubMed=12185539;
 RA Wagner B., Griseier-Wilke I., Wege A.K., Radbruch A., Leibold W.,
 RT "Evolution of the six horse IgH Genes and corresponding ImmunoGenetics 54:1353-1364 (2002).
 RL ImmunoGenetics 199:105-118 (1998).
 RN [3] _
 RN SEQUENCE FROM N.A.
 RX MEDLINE=9717671;
 RA HSSP; P01857; 1HZH;
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF07654;
 DR SMART; SM00407; IgC1_2.
 DR PROSITE; PS50835; Ig_LIKE; 3.
 DR PROSITE; PS00290; Ig_MHC; UNKNOWN_2.
 FT NON_TER 1 1
 FT CHAIN <1 337 immunoglobulin gamma 1 heavy chain constant region.
 SQ SEQUENCE 337 AA; 37438 Mn; A60BFEB01BD1F6 CRC64;

Query Match Score 48.2%; DB 2; Length 337;
 Best Local Similarity 32.8%; Pred. No. 5e-29;
 Matches 113; Conservative 67; Mismatches 120; Indels 45; Gaps 12;

Query Match Score 48.5%; DB 1; Length 326;

QY	23 PTVKLFFHSSCDPREGDAHTSTIQLCLVSGSFPAKVKHVTW---LVDGQEAENLFPYTRPK 78	DR SMART; SMO0407; IGC1; 2.
DB	6 PTKVAPALCGCTISD--SIVVALCCLVSYSFPEVKVWSNGSLTSG--VHTFPSVL--- 57	DR PROSITE; PS00335; IG_LIKE; 2.
DB	79 REGQQTFSLOSEVNITQGOMMSNTYTCVXKGNSIPE-----DSSRKCADSN--P 127	DR PROSITE; PS00390; IG_MHC; 2.
QY	58 -QSSGFYLSMNTVPASTW-TETBYCNVVAASNFVVDKRIEPIPDDNHQKVDNSKCP 115	KW 3D-structure; Direct protein sequencing; Immunoglobulin C region;
DB	126 R-----GVSAVNLSSMNTVPASTW-LPIRKSPPTCLVWVLAPEKGTNLTWASGRPVNH 178	KW Immunoglobulin domain;
QY	116 KCPAPELIGGSPTEIFPPNPKDLMITTPVEVTCVWVDSQENPDYKFKNWMDGVEVRTA 175	FT NCN_TER
DB	179 STRZBEKQNGNTUTVTSTLPVGTRDWIGETYQCRVTHPHBLRALKRSSTKLPGKRLAPE 238	FT DOMAIN
QY	176 TTPKEEEQPNSTYKRVVSLRQIDMSEKPKCKRQALQPIERTTKGRSQEQ 235	FT DOMAIN
DB	239 VMLLPPSPBETGTR-TVTCILRGFYPEISYQWLNNEEDHTGHHTTTRPQKDHEGTDPS 297	FT DOMAIN
QY	236 VVIAHPHDELSKSKVSTCLVDFYPEINEWQSNGSQPELETKYSTQAQQD--SDGS 293	FT DOMAIN
QY	298 FFLYSRMLYNKSWEKGHNUTVTCVYHEALPGSRTITLEKSHYSGN 342	FT DISTUFID
DB	294 YFLYSKLSSVDRNRWQOGTTFTCGVMHEAHN-----HYTQKN 330	FT DISTUFID
QY	GC4 HUMAN STANDARD; PRT; 327 AA.	FT DISTUFID
DB	AC P01861; 21-JUL-1986 (Rel. 01, Created)	FT DISTUFID
DT 21-JUL-1986 (Rel. 01, Last sequence update)	FT DISTUFID	
DT 01-OCT-2004 (Rel. 45, Last annotation update)	FT DISTUFID	
DE 19 Gamma-4 chain C region.	FT DISTUFID	
GN Name=IGHG4;	FT DISTUFID	
OS Homo sapiens (Human)	FT DISTUFID	
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	FT DISTUFID	
CC Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.	FT DISTUFID	
NCBI_TaxID=9606;	FT DISTUFID	
RN [1]	SEQUENCE OF 1-30 AND 81-326.	FT DISTUFID
RX MEDLINE=8315104; PubMed=6299662;	FT DISTUFID	
RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;	FT DISTUFID	
RA Human immunoglobulin subclasses. Partial amino acid sequence of the constant region of a gamma 4 chain.;	FT DISTUFID	
RT Biochem. J. 117:35-47(1970).	FT DISTUFID	
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CC DNA 1:11-18(1981). [2]	FT DISTUFID	
RN SEQUENCE FROM N.A.	FT DISTUFID	
RX MEDLINE=8127438; PubMed=6287432;	FT DISTUFID	
RP Ellision J.W., Berson B.J., Hood L.E.;	FT DISTUFID	
DR "The nucleotide sequence of a human immunoglobulin C gamma 1 gene.", Nucleic Acids Res. 10:1071-1079 (1982).	FT DISTUFID	
DR Genew; HGNC;5528; IGHG4.	FT DISTUFID	
DR MIN; 141130; --.	FT DISTUFID	
DR GO; GO:0005624; C:membrane fraction; NAS.	FT DISTUFID	
DR GO; GO:0003823; F:antigen binding; TAS.	FT DISTUFID	
DR GO; GO:0006955; P:immune response; NAS.	FT DISTUFID	
DR InterPro; IPR007110; Ig-like.	FT DISTUFID	
DR InterPro; IPR003557; Ig CL.	FT DISTUFID	
DR Pfam; PF00047; Ig_MHC.	FT DISTUFID	
DR Pfam; PF00047; Ig; 3.	FT DISTUFID	
QY	RESULT 3	RESULT 4
GC4 HUMAN STANDARD; PRT; 327 AA.	GC1_HUMAN STANDARD; PRT; 330 AA.	
AC P01861; 21-JUL-1986 (Rel. 01, Created)	AC P01861; 21-JUL-1986 (Rel. 01, Created)	
DT 21-JUL-1986 (Rel. 01, Last sequence update)	DT 21-JUL-1986 (Rel. 01, Last sequence update)	
DE 19 Gamma-4 chain C region.	DT 01-OCT-2004 (Rel. 45, Last annotation update)	
GN Name=IGHG4;	DB IG_Gamma-1 chain C region.	
OS Homo sapiens (Human)	OS Homo sapiens (Human)	
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;	OC Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.	
NCBI_TaxID=9606;	NCBI_TaxID=9606;	
RN [1]	RN [1]	
RX MEDLINE=8127438; PubMed=6287432;	RX MEDLINE=8127438; PubMed=6287432;	
RP Ellision J.W., Berson B.J., Hood L.E.;	RP Ellision J.W., Berson B.J., Hood L.E.;	
DR "The nucleotide sequence of a human immunoglobulin C gamma 1 gene.", Nucleic Acids Res. 10:1071-1079 (1982).	DR "The nucleotide sequence of a human immunoglobulin C gamma 1 gene.", Nucleic Acids Res. 10:1071-1079 (1982).	
DR Genew; HGNC;5528; IGHG4.	DR Genew; HGNC;5528; IGHG4.	
DR MIN; 141130; --.	DR MIN; 141130; --.	
DR GO; GO:0005624; C:membrane fraction; NAS.	DR GO; GO:0005624; C:membrane fraction; NAS.	
DR GO; GO:0003823; F:antigen binding; TAS.	DR GO; GO:0003823; F:antigen binding; TAS.	
DR GO; GO:0006955; P:immune response; NAS.	DR GO; GO:0006955; P:immune response; NAS.	
DR InterPro; IPR007110; Ig-like.	DR InterPro; IPR007110; Ig-like.	
DR InterPro; IPR003557; Ig CL.	DR InterPro; IPR003557; Ig CL.	
DR Pfam; PF00047; Ig_MHC.	DR Pfam; PF00047; Ig_MHC.	
DR Pfam; PF00047; Ig; 3.	DR Pfam; PF00047; Ig; 3.	

RL	Biochemistry 9:3161-3170(1970).	DR	PDB; 1D6V; X-ray; H=1-101.
RN	[3]	DR	PDB; 1DN2; X-ray; A/B=1-120-326.
RP	SGCUNINE OF 136-329 (EU).	DR	PDB; 1EAK; X-ray; A/B=106-329.
RP	SGCUNINE 71064025; PubMed=5530842;	DR	PDB; 1ECK; X-ray; A/B=106-329.
RX	Rutishauser U., Cunningham B.A.; Bennett C., Konigsberg W.H.,	DR	PDB; 1FC2; X-ray; D=106-329.
RA	Edelman G.M.;	DR	PDB; 1FCC; X-ray; A=121-326.
RA	"The covalent structure of a human gamma G-immunoglobulin 8 amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";	DR	PDB; 1HZH; X-ray; H/K=1-330.
RT	Biochemistry 9:3171-3181(1970).	DR	PDB; 1IZZ; X-ray; B/D=1-103.
RT	acid sequence of heavy-chain cyanogen bromide fragments H5-H7."	DR	PDB; 1JIS; X-ray; A/B=107-330.
RL		DR	PDB; 1LIX; X-ray; A/B=107-330.
RN		DR	PDB; 1L6X; X-ray; A=120-326.
RP	SEQUENCE (MYELOMA PROTEIN NIE).	DR	PDB; 1OQS; X-ray; A/B=119-330.
RX	MDNSTING L.H., Hilschmann N.; Pubmed=26475;	DR	PDB; 1RCS; X-ray; H=1-103.
RA	Postling H., Hilschmann N.;	DR	Genew; HGNC:5525; IgG1.
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Niel). III. The cymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."	DR	MIM; 147100; C:membrane fraction; NAS.
RT	RT	DR	GO; GO:0005624; P:antigen binding; TAS.
RT	RT	DR	GO; GO:0003823; P:immune response; TAS.
RT	RT	DR	InterPro; IPR01710; Ig-like.
RN		DR	InterPro; IPB003006; Ig_MHC.
RP	SEQUENCE (MYELOMA PROTEIN KOL) AND DISULFIDE BONDS.	DR	Pfam; PF00047; ig_3.
RX	MEDLINE=93209131; PubMed=684994;	DR	PROSITE; PS50835; Ig-LIKE; 3.
RA	Schmidt W.E., Jung H.-D., Paul W., Hilschmann N.;	DR	PROSITE; PS00290; Ig_MHC; 2.
RA	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.;"	KW	3D-structure; Direct protein sequencing; Glycoprotein;
RT	RT	KW	Immunoglobulin C region; Immunoglobulin domain.
RL	Intrachain disulfide bonds."	FT	NON_TER 1 1
RN	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).	FT	DOMAIN 1 1
[6]		FT	CH1.
RP	DISULFIDE BONDS.	FT	DOMAIN 1 1
RX	MEIDLINE=71064027; PubMed=4923144;	FT	CHinge.
RA	Gall W.E., Edelman G.M.;	FT	DOMAIN 1 1
RA	"The covalent structure of a human gamma G-immunoglobulin. X. Structure of crystallized monoclonal immunoglobulin IgG1 KOL, I;"	FT	CH2.
RT	Intrachain disulfide bonds."	FT	DOMAIN 2 2
RT	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).	FT	CH3.
RN		FT	DISULFID 27 83
RN		FT	Interchain (with light chain).
RP	DISULFIDE BONDS.	FT	DISULFID 103 103
RX	MEIDLINE=770267; PubMed=1002129; PMID=4923144;	FT	Interchain (with heavy chain).
RA	Dreker L., Schwarz J., Reichel W., Hilschmann N.;	FT	DISULFID 109 109
RT	"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Niel). I: purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."	FT	Interchain (with heavy chain).
RT	Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).	FT	DISULFID 112 112
RN		FT	Interchain (with heavy chain).
[7]		FT	DISULFID 144 204
RP	DISULFIDE BONDS.	FT	DISULFID 250 308
RX	MEIDLINE=770267; PubMed=1002129; PMID=4923144;	FT	N-linked (GlcNAc- : -).
RA	Deisenhofer J., Hilschmann N.;	FT	K->P (in G1M(1)) marker.
RT	"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.5-A resolution."	FT	/FTId=VAR_003886
RT	RT	FT	D -> E (in G1M(non-1) marker).
RT	RT	FT	/FTId=VAR_003887
RL	Biocchem 20:1236-1237(1981).	FT	L -> M (in G1M(non-1) marker).
RN		FT	/FTId=VAR_003888.
RP	X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).	FT	STRAND 23 24
RX	MEDLINE=81208100; PubMed=2366608;	FT	STRAND 26 33
RA	Deisenhofer J.;	FT	STRAND 38 38
RT	"Crystallographic refinement and atomic models of a human Fc fragment and its complex with fragment B of protein A from Staphylococcus aureus at 2.9- and 2.5-A resolution."	FT	STRAND 41 41
RT	RT	FT	TURN 42 45
RT	RT	FT	TURN 48 49
RL	-!- MISCELLANEOUS: Nie has the G1M(17) allotypic marker, 97-K, and the G1M(1) markers, 229-D and 241-L. KOL and EU sequences have the G1M(3) marker and the G1M (non-1) markers.	FT	STRAND 50 52
CC	-!- MISCELLANEOUS: Nie also differs in the amidation states of 35,	FT	TURN 57 58
CC	-!- 116-198, 269 and 272.	FT	STRAND 59 61
CC	-!- MISCELLANEOUS: EU also differs in the amidation states of residues 155, 166, 177, 195, 269, and 272 and in the order of residues 268-272.	FT	TURN 62 71
CC	-!- MISCELLANEOUS: KOL also differs in the amidation states of residues 198, 267 and 272.	FT	STRAND 73 75
CC		FT	TURN 76 78
CC		FT	STRAND 82 87
CC		FT	TURN 88 91
CC		FT	STRAND 92 97
CC		FT	TURN 102 103
CC		FT	STRAND 122 126
CC		FT	TURN 136 137
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	FT	STRAND 141 149
CC		FT	STRAND 157 162
CC		FT	TURN 163 164
CC		FT	STRAND 165 167
CC		FT	TURN 171 172
CC		FT	STRAND 176 177
CC		FT	TURN 179 180
DR	PIR; J00228; AAC2527.1; ALT_INIT.	FT	STRAND 183 190
DR	A91433; GHGU.	FT	TURN 193 197
DR	PDB; 1A77; X-ray; H=1-103.	FT	HELIX 198 199
DR	PDB; 1D5B; X-ray; B/H=1-101.	FT	TURN 202 207
DR	PDB; 1D5I; X-ray; H=1-101.	FT	STRAND 207

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CC EMBL; M13804; AAA41376.1; ALT_INIT.

CC PIR; PS0019; PS0019.

CC PDB; 1IIA; X-RAY; C=98-321, D=98-322.

CC DR; 1IIA; X-RAY; A,B=98-322.

CC Intertro; IPRO003597; Ig_C1.

CC InterPro; IPRO003006; Ig_MHC.

CC Pfam; PF00047; Ig_2.

CC SMART; SM00407; IgCl.

CC PROSITE; PS50035; Ig_LIKE_3.

CC PROSITE; PS00290; Ig_MHC_1.

CC 3D-structure; Immunoglobulin C region; Immunoglobulin domain; Repeat.

RW KW

FT FT TURN 209 210

FT STRAND 215 219

FT STRAND 227 227

FT STRAND 230 234

FT HELIX 238 242

FT STRAND 245 256

FT STRAND 261 266

FT TURN 267 268

FT STRAND 269 270

FT STRAND 274 276

FT STRAND 280 281

FT TURN 283 284

FT STRAND 287 295

FT HELIX 297 301

FT TURN 302 303

FT STRAND 306 311

FT TURN 313 314

FT HELIX 316 318

FT STRAND 319 324

SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;

Query Match Best Local Similarity 24.5%; Score 454; DB 1; Length 330; Pred. No. 7.7-27; Mismatches 17; Indels 36; Gaps 12;

Matches 117; Conservative 57; Mis matches 130; Indels 36; Gaps 12;

QY 22 PPTVKLFHSSCDPGRDAHTSTIQLCLVSGFSPAKVHYTW---IVDQEAENLFPTTRP 77

Db 6 PSVFLPLAPSSKSTSG---GTAALGCLVDFPFEPVPTVSNSGALTSG---VHTFPAVL-- 57

QY 78 KREGGOTFLQSENNITQGMNSNTYCHXENGTSFBE-----DSSRKC---A 123

Db 58 --QSSGLYKLVSSVTVPSSS-LGTRQTYICNVNHEKPSNTVKDVKEPKSDCKHTTCPCPA 114

QY 124 DSNPFGVASYLRSRSPSPD-LFTRGPSPPTCLVYDABKGTVNLWSRASGKPVNHSRK 182

Db 115 PELLGGPVFLFPKPKDTLMISRTPETCVVVDVSHEDPEYKENVYDGVVEHNAKTKP 174

QY 183 EERKONGNLTVTSTLPGVTRDWEGETTQCRVTHPHLPRLMRSTLKLPGKRLAPELLM 242

Db 175 REEYNSNTYRVSVLTVHQDWLNGKEYRKCVSNKALAPIEXTISAKGQPREPOVTL 234

QY 243 PPSPSEE-TCTTTRVTCILRGFYSEIYSTOWLTNEEDHTGHETTTIPQKDHTGTDPSFELY 301

Db 235 PPSPDELTKNQVSITCLRGFYSEIYSTOWLTNEEDHTGHETTTIPQKDHTGTDPSFELY 290

QY 302 SRMLVNKSTWEKENLVTQCRVHAEALPGSRTLEKSLHYSG 341

Db 291 SKLUTVDKSRWQCNVFSCSVMEHALNHYT-QKSLSLSPG 329

RESULT 5

GCA_RAT ID_GCA_RAT STANDARD; PRT; 322 AA.

RN [1] NCBI_TaxID=10116; STANDARD; PRT; 322 AA.

RP SEQUENCE FROM N.A.

AC F20760;

DT 01-FEB-1991 (Rel. 17, Created)

DT 01-FEB-1991 (Rel. 17, Last sequence update)

DE 19 Gamma-2A chain C region.

OS Rattus norvegicus (Rat)

CC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Rodentia; Muridae; Murinae; Rattus.

OX RN [1]

RP SEQUENCE FROM N.A.

AC MEDLINE:89222738; PubMed=3149946;

RX Brueggemann M.; "Evolution of the rat immunoglobulin gamma heavy-chain gene family." Gene 74:473-482 (1988).

RE 74:473-482 (1988).

CC !- SIMILARITY: Contains 3 immunoglobulin-like domains.

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CC EMBL; P01810; (Rel. 01, Created)

CC DT 21-JUL-1986 (Rel. 01, Last sequence update)

CC DT 05-JUL-2004 (Rel. 44, Last annotation update)

CC DE 19 Gamma chain C region.

OS Oryctolagus cuniculus (Rabbit)

OC Mammalia; Eutheria; Mectzoa; Chordata; Craniata; Vertebrata; Buteleostomi; Lagomorpha; Leporidae; Oryctolagus.

OX RN [1]

RP SEQUENCE FROM N.A.

SEQUENCE_OF 134-226.
MEDLINE=7506072; PubMed=4429665;
RX
RA Tracey D.E.; Cebray J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
antibodies";
RT Biochemistry 13:4796-4803 (1974).
RN [5]
SEQUENCE_OF 227-311.
RX MEDLINE=7505672; PubMed=4609467;
RA Trischmann T.M.; Cebray J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
antibodies";
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE_BONDS.
RX MEDLINE=71058474; PubMed=4922544;
RA Oliveira B.; Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RL Biochemistry 10:26-31(1971).
CC -; MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC 13 inbred guinea pigs.
DR PIR; A94553; G2GP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR00306; Ig_NHC.
DR Pfam; PF00047; Ig_C1_2.
DR SMART; SMO0407; IgC1_2.
DR PROSITE; PS50835; IG-LIKE_3.
DR PROSITE; PS00290; Ig_NHC_1.
DR Direct protein sequencing; Glycoprotein; Immunoglobulin C region;
KW Immunoglobulin domain.
NON_TER 1 1
FT DISULFID 16 16
FT DISULFID 28 79
FT DISULFID 105 105
FT DISULFID 107 107
FT DISULFID 110 110
FT DISULFID 142 202
FT CARBOHYD 178 308
FT DISULFID 248 329
SQ SEQUENCE AA; MW; Score 424.5; DB 1; Length 329;
Best Local Similarity 33.2%; Pred. No. 1.4e-24;
Matches 115; Conservative 52; Mismatches 136; Indels 43; Gaps 13;

Query Match 19. TIPPTVLFHSSCDPREGDAHSTIOLCLVSGFSPAKVHTW---LVDGQEAENLFPYV 74
Best Local Similarity 33.2%; Pred. No. 1.4e-24;
Matches 115; Conservative 52; Mismatches 136; Indels 43; Gaps 13;

Query 121 -KC-ADSNPRGVAYSLRSRSPSPD-LFIRKSPITCLVYLAPSKGTVNLTISRAGKPV- 176
DB 4 TTPSPVPLAASCVDTSS---SMMTLUSCLVGYFPEPVTVKNSGALTSG---VHTFFAV 57

Query 75 TRPKREGQQTSLOSEVNITQOGWMSNTYTCVHKHNGSIFEDSSR----- 120
DB 58 LQ----SGLYSLTSMTVP----SSQRATCNVAHPASSTKVDKTVEPIRTPZBPCCTC 107

Query 177 NHSTRKEEKNRNETLTVTSLPVGTRDMIEGETYQCRVTHPHLPALMRSTTKLPGKRLA 236
DB 167 NAETKPRVQEYNTTFRVESVLPIQHQDWLRGEFKCKVNNALPAJETKISKTGKAPRM 226

Query 237 PEVYMLPPSPEETGTR-TVTCLJRGFPEVSEIQLFNNEEDHTGHHTTRQDHDGT 295
DB 227 PDVYTLPPSRDELSSKSRYSVTCHINFPADLIVEWASNRVPUSEKEYKNTPPIED-AD 284

Query 236 PSFLFLYSMLVNVSIWEGNLVTCRVEHALPGSRTEKSHLYHAG 341
DB 285 GSFLFLYSLRKLTVDKSAWDGTVTCWSMHALHNHT-QKAISRSRPG 329

GCAB_MOUSE STANDARD PRT; 335 AA.
ID GCAB_MOUSE ID 01. 01. Created
AC 2018-04-21-JUL-1986 (Rel. 01. Last sequence update)
DT 21-JUL-1986 (Rel. 01. Last annotation update)
DT 01-OCT-2004 (Rel. 45. Last sequence update)
DE 19 gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
NCBI_TaxID=10090; OX [1]
RN SEQUENCE FROM N.A.
RP [6]
RC STRAIN=S2037BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H.; Bachwell A.L.M.; Mueller-Hill B.; Baltimore D.; RT "Multiple differences between the nucleic acid sequences of the IgG2aa and IgG2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4195-4199(1981).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=82037777; PubMed=6794027;
RA Deenin M.J.; Lauwers M.; Strosberg A.D.; BA "Multiple amino acid substitutions between murine gamma 2a heavy chain regions of IgG1 and IgG1 allotypic forms.";
RT Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035(1981).
CC -; SUBCELLULAR LOCATION: Secreted (Potential).
CC -; ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoID=PI01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoID=PI01865-1; Sequence=External;
CC CC -; MISCELLANEOUS: The sequence differs from that of the a allele, from BALB/c mice, at 15% of the positions.
CC -; SIMILARITY: Contains 3 immunoglobulin-like domains.
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EMBL; J00079; ; NOT_ANNOTATED_CDS.
PIR; A01153; G2MSAB.
PDB; 1BQG; X-ray; B=1-101.
PDB; 1HH6; X-ray; B=1-101.
PDB; 1HH9; X-ray; B=1-101.
PDB; 1HH6; X-ray; B=1-101.
InterPro; IPRO07110; Ig-1-like.
InterPro; IPRO03006; Ig_MHC.
PFam; PF00047; Ig_2.
PROSITE; PS50835; Ig_LIKE_3.
DR PROSITE; PS00040; Ig_MHC_1.
DR 3D-structure; Alternative_splicing; Direct_protein_sequencing;
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.

FT DOMAIN 1 98 Ig-like 1.
FT DOMAIN 6 126 Ig-like 2.
FT DOMAIN 234 330 Ig-like 3.
FT STRAND 4 4
FT STRAND 7 11
FT STRAND 22 33
FT STRAND 38 41
FT STRAND 42 45
FT STRAND 46 46
FT TURN 48 49
FT STRAND 50 52
FT STRAND 56 58
FT STRAND 59 60

FT	STRAND	61	71	RP	SEQUENCE (MYELOMA PROTEIN MOPC 21).			
FT	TURN	72	77	RX	MEDLINE=70242288; PubMed=98524;			
FT	STRAND	81	86	RA	Adetugbo K.;			
FT	HELIIX	87	89	RT	"Evolution of immunoglobulin subclasses. Primary structure of a murine			
FT	TURN	90	90	RL	myeloma gamma chain."			
FT	STRAND	91	96	J. Biol. Chem.	253:6068-6075 (1978).			
SQ	SEQUENCE	335 AA;	36596 MW;	RN [5]	RN [5]			
Query Match	Score 421; DB 1; Length 335;			DISULFIDE BONDS (MOPC 21)				
Best Local Similarity	22.7%; Pred. No. 2, 7e-24;			MEIDLINE=7008889; PubMed=5073237;				
Matches 105; Conservative	54; Mismatches .124; Indels .50; Gaps .9;			RA	The disulphide bridges of a mouse immunoglobulin G1 protein."			
QY	36 GDAHSTIQQLCLVGSFSPAKRYHTW---LVDGQEAEILFPTVTRPKREGGOTFSLOSEV 91			RL	Biochim. J. 126:1837-850 (1972).			
Db	17 GTTSSSVTIGCLVKGKFPPBVTILWNSSSLSSGVH-----TFPALLQSGLYLUSSV 68			CC	-!- SUBCELLULAR LOCATION: Secreted.			
QY	92 NITQGOMWSNTTYTCHVKGNSLEFDSSRKCADSNPR-----			CC	-!- ALTERNATIVE PRODUCTS:			
Db	69 TVTNTNW PSQTITCNVHPAS ---SKVDKKIEPRVPTONPCPHQRVPPCAAFDLL 123			CC	Event-Alternative splicing; Named isoforms=2;			
QY	129 -GVSAYLRSRPSPPD-LFRKSPTITCLNDLAPSQKFTVNLTISRASESKPVNHSSTRKEKQ 186			CC	Name=secreted;			
Db	124 GGPEVFFPPKPKDYLMSLSPVPTCYVVDSDPEQISFEVNNYVEVHTAQOTQTHRED 183			CC	IsOid=P01868-1; Sequence=Displayed;			
QY	187 RNGHLTVTSTPLPVGRDWEGETYQCRVTHPHILPALARSTIKLPGKRLAPEVYMPPPSP 246			CC	Note=May be the major isoform;			
Db	184 YNSTLTVYVSAPIQHQDNMSGKFKCKVNRAPSPPIEKTSKPRGPVRAPAOVYVLLPPA 243			CC	Name=Membrane-bound;			
QY	247 EB-TGTTTIVTCJLRGFYFSEISIVQMLNEEDHTGHHTTTRPQDKDHGTDPSFLYSRML 305			CC	IsOid=P01869-1; Sequence=External;			
Db	244 EEMTKKEFSLTCMTGFPAPAEIADVWTNGTREQNYNTATVYD---SDGSYFMYSKLR 299			CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
QY	306 VNKSIIWEKGNLVNTCRVWHEELALP---SPTLEKSL 336			CC	between the Swiss Institute of Bioinformatics and the EMBL Outstation			
Db	300 VQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			CC	the European Bioinformatics Institute. There are no restrictions on its			
QY	301 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			CC	use by non-profit institutions as long as its content is in no way			
QY	302 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			CC	modified and this statement is not removed. Usage by and for commercial			
QY	303 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			CC	entities requires a license agreement (see http://www.isb-sib.ch/announce/)			
QY	304 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			CC	or send an email to license@isb-sib.ch.			
QY	305 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			CC	EMBL: J00453; AAB5656_1; -.			
QY	306 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	EMBL: J00453; AAB5656_1; -.			
QY	307 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	PIR: A02159; QIMS.			
QY	308 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GlycoSuiteDB; P01868; -.			
QY	309 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	MGI: MGI_36446; IgN-4.			
QY	310 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GO: 000242578; C: Immunoglobulin complex, circulating; IDA.			
QY	311 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GO: 0003823; F: antigen binding; IDA.			
QY	312 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GO: 001373; F: antibody-dependent cellular cytotoxicity; IDA.			
QY	313 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GO: 0001788; F: complement activation classical pathway; IDA.			
QY	314 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GO: 0004230; P: defense response mechanism (sensu vertebrata); IDA.			
QY	315 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GO: 0050728; P: negative regulation of inflammatory response; IDA.			
QY	316 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	DR GO: 0006910; P: phagocytosis, engulfment; IDA.			
QY	317 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	GO: 0050776; P: positive regulation of immune response; IDA.			
QY	318 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	DR GO: 0050729; P: positive regulation of inflammatory response; IDA.			
QY	319 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	DR GO: 0050766; P: positive regulation of phagocytosis; IDA.			
QY	320 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	DR InterPro: IPR007110; Ig-like.			
QY	321 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	DR InterPro: IPR03006; Ig-MHC.			
QY	322 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	Pfam: PF00047; Ig.			
QY	323 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	PROSITE: PS500335; Ig_LIKE; 3.			
QY	324 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			DR	PROSITE: PS00290; Ig_MHC; 1.			
QY	325 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			KW	Alternative splicing; Direct protein sequencing; Glycoprotein;			
QY	326 SPTLEKSLVQKSTTWERSSLFACSVVHEVNLHTRKTSRL 333			KW	Immunoglobulin C region; Immunoglobulin domain.			
RESULT 11				FT	NON_TER	1	1	CH1.
GC1_MOUSE	STANDARD;	PRT;	324 AA.	FT	DOMAIN	1	97	Hinge.
ID	P01868;			FT	DOMAIN	98	110	
AC				FT	DOMAIN	111	217	
DT	21-JUL-1986 (Rel. 01, Created)			FT	DOMAIN	111	324	CH2.
DT	21-JUL-1986 (Rel. 01, Last sequence update)			FT	DISULFID	27	82	Interchain (with a light chain).
DT	05-JUL-2004 (Rel. 44, Last annotation update)			FT	DISULFID	102	104	Interchain (with a heavy chain).
DE	19 gamma-1 chain C region secreted form.			FT	DISULFID	104	107	Interchain (with a heavy chain).
OS	Mus musculus (Mouse).			FT	DISULFID	107	109	Interchain (with a heavy chain).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus. NCBI_TaxID=10090;			FT	DISULFID	138	198	N-linked (GlcNAc. . .).
OX				FT	CARBOHYD	174	174	/FTid=CAR_000055.
RN	SEQUENCE FROM N.A. MEDLINE=80045036; PubMed=115593;			FT				
RX	Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Kato Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.; "Immunglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid." Gene 9:87-97(1980). [3]			FT				
RX	SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C). MEDLINE=80202559; PubMed=6169732;			FT				
RA	Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T., Takahashi N., Kato Y., Takahashi N., Kataoka T., Shimizu A., Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.; "Immunglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid." Gene 9:87-97(1980). [3]			FT				
RX	SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21). MEDLINE=8001237; PubMed=113776;			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RX	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Acids Res. 6:3305-3321(1979). [4]			FT				
RA	Rogers J., Clarke P., Salter W.; "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain." Nucleic Ac							

SMART; SM00407; IgG1; 2.
 DR PROSITE; PS5035; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW 3D-structure; Immunoglobulin C region; Immunoglobulin domain; Repeat.

PT	NON-TER	1	1	Ig-like 1.
PT	DOMAIN	6	98	Ig-like 1.
PT	DOMAIN	121	220	Ig-like 2.
PT	DISULFID	15	325	Ig-like 3.
PT	DISULFID	27	82	Interchain (with a light chain).
PT	DISULFID	107	107	Interchain (with a heavy chain).
PT	DISULFID	110	110	Interchain (with a heavy chain).
PT	DISULFID	112	204	Interchain (with a heavy chain).
PT	DISULFID	144	204	Interchain (with a heavy chain).
PT	DISULFID	250	308	
PT	STRAND	4	4	
PT	STRAND	7	11	
PT	STRAND	22	33	
PT	STRAND	38	41	
PT	HELIX	42	44	
PT	TURN	45	45	
PT	STRAND	46	46	
PT	STRAND	50	52	
PT	STRAND	56	56	
PT	TURN	59	60	
PT	STRAND	62	71	
PT	TURN	72	77	
PT	STRAND	81	86	
PT	HELIX	87	89	
PT	TURN	90	90	
PT	STRAND	91	96	
SQ	SEQUENCE	330 AA:	36389 MW;	B84361C545A6864 CRC64;

Query Match 21.3%; Score 395.5; DB 1; Length 330;

Best Local Similarity 31.7%; Pred. No. 2; e=22; Mismatches 12; Indels 45; Gaps 12;

Matches 104; Conservative 55; Misconservative 49; Score 395.5; DB 1; Length 330;

QY	40	STIQLCLVSGFSPAKWVHTW	--LVDQQAENLFPYTRPKREGQQTSLOSEVNITQ	95
Db	21	SSVTIGCLVGRGYFPBPVTLTWNCSLSG	--VHTFPAVLQ---SDLYTLLSSSVTVTS	72
QY	96	GQWMSNNTTCVWKGNSIFEDBSRKCAPDSNPGVSA	--YLSRPSPP--	140
Db	73	STW-PSOS-LTCVTAHPAS	--STKVDKKIEPRGPTIKPCPCKCPAPNLGGPSVFIFF	127
QY	141	-----DLFTRKSPSPITICLVVDIAFLASKGVNLTWRSASSGPVNTHSTRKEKORGTLTVTS	195	
Db	128	PKIDVLMISLSPVTVTVDSEDDPVQISWVDETEVHQAQTQHREDNSTRVVS		187
QY	196	TLPVGTRDWIEGETYQCRRVTPHLPLRALMRSITKLPGKRLAPEVYMLPPSPEETGTR	--	253
Db	188	ALPIQHQDMWSGKEFKCKVNNKOLPAPERTISKPKGSVRAQVyyVLP-PEBEMTKQV	246	
QY	254	TWTCULRGTFPSPELSVQUNNNEEDHTGHITTRPOQDHGTFDPSFLYSLVWNSIWEK		313
Db	247	TLTmAVTDMPEDIVVENTNGKTEL-NYQNTEPVLID--SDGSYFMYSKLVEKRNWVE		302
QY	314	GNYLTCRYTHEALPGSRLEKSHYSAG	341	
Db	303	RNSYSCSCTYHEGLHNHHT-TKSFSSRTPG		329

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RESULT 2
PCT-US5-13795-2
 ; Sequence 2, APPLICATION PC/TUSS9513795
 ; GENERAL INFORMATION:
 ; APPLICANT: HOLLIS, GREGORY F.
 ; ADDRESS: 126 E. LINCOLN AVENUE; P.O. BOX 2000
 ; CITY: RAHWAY
 ; STATE: NEW JERSEY
 ; COUNTRY: USA
 ; ZIP: 07065-0907
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/13795
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: CARTY, CHRISTINE E.
 ; REGISTRATION NUMBER: 36,099
 ; REFERENCE/DOCKET NUMBER: 19211Y
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (908) 594-6734
 ; TELEFAX: (908) 594-4720
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 426 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

Query 18 VTIIPPTVKLFHSSCDPRGDAHTSILCLUSGFSPAKVHYTWLQOEAEENLFPTYTRP
 Best Local Similarity 53.3%; Score 989; DB 5; Length 426;
 Matches 185; Conservation 53; Mismatches 84; Indels 4; Gaps 3;

Db 102 SPFLFRKSPITCLVVDLAPSKGTVNLWSRASGPVNHSRKDEARKCSESDRGVTSYLSPP 220

Db 162 TKEGNVT-STHSELNITQGEWSQXTYTQGFTPKDEARKCSESDRGVTSYLSPP 220

Qy 138 SPFLFRKSPITCLVVDLAPSKGTVNLWSRASGPVNHSRKDEARKCSESDRGVTSYLSPP 197

Db 221 SPFLYHKAPKITCHLVDLATMEG-MNLTYRESKEPVNGPLNKDKHNGTIVTSTL 279

Qy 198 PYGTRDWEGETYQCRVTHPHLPRLMRSTKLPGKRLAPAEVYMLPPSPBTGTTR-TV 255

Db 280 PYNTNDWEGETYQCRVTHPHLPKD'TRSIAKAPGRAPPVYLFLPPEEQGTVKDRVTL 339

Qy 256 TCLIRGFPSEISVQWLFNNNEEDHTGHHTTRPQDHTGTDPSFFLYSRMLYNKSWEKG 315

Db 340 TCLIQNFPADISVQWLRNDSPLOTOYTIGPHKVSGRPAFFSRLEVSVDWEQRN 399

Qy 316 LVTCRVTHEALGSRTELEKSLHYSG 341

Db 400 KFTCQVTHEALGSRSLQKWWSKTPG 425

RESULT 3
US-09-479-614-14
 ; Sequence 14, Application US/09479614
 ; GENERAL INFORMATION:
 ; APPLICANT: McCall, Catherine
 ; TITLE OF INVENTION: Feline Immunoglobulin E Molecules and Related Methods
 ; FILE REFERENCE: P-1047
 ; CURRENT APPLICATION NUMBER: US/09/479,614
 ; CURRENT FILING DATE: 2000-01-07
 ; EARLIER APPLICATION NUMBER: 60/115,033
 ; EARLIER FILING DATE: 1999-01-07
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 14
 ; LENGTH: 431
 ; TYPE: PRT
 ; ORGANISM: Felis catus
 ; US-09-479-614-14

Query Match 52.4%; Score 972; DB 4; Length 431;
 Best Local Similarity 56.7%; Pred. No. 5.9e-86;
 Matches 185; Conservation 52; Mismatches 85; Indels 4; Gaps 4;

Qy 18 VTIIIPPTVKLFHSSCDPRGDAHTSILCLUSGFSPAKVHYTWLQOEAEENLFPTYTRP 77
 Db 107 MNPIIPPTVKLFHSSCDPRGDAHTSILCLUSGFSPAKVHYTWLQOEAEENLFPTYTRP 166

Qy 78 KREGGQTTSLOSEVNITQGQMSNTYTCVYKHNGSFEDSSRKCADSNPRGVSAYLSPR 137

Db 167 KQGKVTT-STHSELNITQGQMSNTYTCVYQGFFEDHARKCTESDPGVSTYLSPP 225

Qy 138 SPFLFRKSPITCLVVDLAPSKGTVNLWSRASGPVNHSRKDEARKCSESDRGVTSYLSPP 197

Db 226 SPFLYHKAPKITCHLVDLATMEG-MNLTYRESKEPVNGPLNKDKHNGTIVTSTL 284

Qy 198 PYGTRDWEGETYQCRVTHPHLPRLMRSTKLPGKRLAPAEVYMLPPSPBTGTTRP
 Best Local Similarity 53.3%; Score 989; DB 5; Length 426;
 Matches 185; Conservation 53; Mismatches 84; Indels 4; Gaps 3;

Db 102 SPFLFRKSPITCLVVDLAPSKGTVNLWSRASGPVNHSRKDEARKCSESDRGVTSYLSPP 161

Qy 78 KREGGQTTSLOSEVNITQGQMSNTYTCVYQGFFEDHARKCTESDPGVSTYLSPP 137

Db 162 TKEGNVT-STHSELNITQGEWSQXTYTQGFTPKDEARKCSESDRGVTSYLSPP 220

Qy 138 SPFLFRKSPITCLVVDLAPSKGTVNLWSRASGPVNHSRKDEARKCSESDRGVTSYLSPP 197

RESULT 4
US-09-479-614-2
 ; Sequence 2, Application US/09479614
 ; General Information:
 ; APPLICANT: McCall, Catherine
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Weber, Eric
 ; REGISTRATION NUMBER: 657372
 ; REFERENCE/DOCKET NUMBER: P-1047
 ; TELEPHONE: (908) 594-6734
 ; TELEFAX: (908) 594-4720
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 426 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein

Query 18 VTIIPPTVKLFHSSCDPRGDAHTSILCLUSGFSPAKVHYTWLQOEAEENLFPTYTRP
 Best Local Similarity 56.7%; Score 989; DB 5; Length 426;
 Matches 185; Conservation 53; Mismatches 84; Indels 4; Gaps 3;

Db 102 SPFLFRKSPITCLVVDLAPSKGTVNLWSRASGPVNHSRKDEARKCSESDRGVTSYLSPP 161

Qy 316 LVTCRVTHEALGSRTELEKSLHYSG 341

Db 405 KFTCQVTHEALGSRSLQKWWSKTPG 430

RESULT 7
US-08-232-539D-56
Sequence 56, Application US/08232539D
Patent No. 5965709
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: IgE Antagonists
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232, 539D
FILING DATE: 21-Apr-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/178583
FILING DATE: 07-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/744768
ATTORNEY/AGENT INFORMATION:
NAME: Svoboda, Craig G.
REGISTRATION NUMBER: 39, 044
REFERENCE/DOCKET NUMBER: P0718P3
TELECOMMUNICATION INFORMATION:
FILING DATE: 14-AUG-1991
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 56:
SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-232-539D-56

Query Match 31.2%; Score 579; DB 2; Length 113;
Best Local Similarity 98.2%; Pred. No. 1.3e-48;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 122 CADSNPROVAYLSRPPFDLIRKSPTCLVLDAPSCKTNLTWSRASGKPVNHSFR 181
Db 1 CADSNPROVAYLSRPPFDLIRKSPTCLVLDAPSCKTNLTWSRASGKPVNHSFR 60

Query Match 31.2%; Score 579; DB 2; Length 113;
Best Local Similarity 98.2%; Pred. No. 1.3e-48;
Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 182 KEEKORNGLTIVTSLPLPGTRWIEGTQCRVTHFLPRALMRSTTKSG 232
Db 61 KEEKORNGLTIVTSLPLPGTRWIEGTQCRVTHFLPRALMRSTTKSG 111

RESULT 8
US-08-466-163B-1
Sequence 1, Application US/08466163B
Patent No. 632509
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
APPLICANT: Jardieu, Paula M.
TITLE OF INVENTION: Immunoglobulin Variants
FILE REFERENCE: P018P21D1
CURRENT FILING DATE: 1995-06-06
PRIOR APPLICATION NUMBER: US 08/405, 617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185, 899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/05860
PRIOR FILING DATE: 1993-08-14
PRIOR APPLICATION NUMBER: US 07/879, 495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744, 768
PRIOR FILING DATE: 1991-08-14
SEQ ID NO 1
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-802-096-1

RESULT 9
US-09-802-096-1
Sequence 1, Application US/09802096
Patent No. 6685339
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
FILE REFERENCE: P0718PC3US
CURRENT FILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: US 08/405, 617
PRIOR FILING DATE: 1995-03-15
PRIOR APPLICATION NUMBER: US 08/185, 899
PRIOR FILING DATE: 1994-01-26
PRIOR APPLICATION NUMBER: PCT/US92/05860
PRIOR FILING DATE: 1993-08-14
PRIOR APPLICATION NUMBER: US 07/879, 495
PRIOR FILING DATE: 1992-05-07
PRIOR APPLICATION NUMBER: US 07/744, 768
PRIOR FILING DATE: 1991-08-14
SEQ ID NO 1
LENGTH: 109
TYPE: PRT
ORGANISM: Homo sapiens
US-09-802-096-1

Query Match 29.6%; Score 548.5; DB 3; Length 109;
Best Local Similarity 97.3%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 124 DSNPRGVAYLSRSPSPFDLIRKSPTCLVLDAPSCKTNLTWSRASGKPVNHSFR 183
Db 1 DSNPRGVAYLSRSPSPFDLIRKSPTCLVLDAPSCKTNLTWSRASGKPVNHSFR 60

Query Match 29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.3%; Pred. No. 1.1e-45;
Matches 106; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

Qy 184 EKQRNGLTIVTSLPLPGTRWIEGTQCRVTHFLPRALMRSTTKPG 232
Db 61 EKQRNGLTIVTSLPLPGTRWIEGTQCRVTHFLPRALMRSTTKSG 108

RESULT 10
US-09-802-077-1
Sequence 1, Application US/09802077
Patent No. 6693472
GENERAL INFORMATION:
APPLICANT: Jardieu, Paula M.
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)

FILE REFERENCE: P0718P2C2US
 CURRENT APPLICATION NUMBER: US/09/802,077
 CURRENT FILING DATE: 2001-05-08
 PRIOR APPLICATION NUMBER: US 08/405,617
 PRIOR FILING DATE: 1995-03-15
 PRIOR APPLICATION NUMBER: US 08/185,899
 PRIOR FILING DATE: 1994-01-26
 PRIOR APPLICATION NUMBER: PCT/US92/06860
 PRIOR FILING DATE: 1992-08-14
 PRIOR APPLICATION NUMBER: US 07/879,495
 PRIOR FILING DATE: 1992-05-07
 PRIOR APPLICATION NUMBER: US 07/879,495
 PRIOR FILING DATE: 1992-05-07
 NUMBER OF SEQ ID NOS: 64
 SEQ ID NO 1
 LENGTH: 1.09
 TYPE: PRT
 ORGANISM: Homo sapiens
 US -09-802-077-1

RESULT 11
 US-08-232-539D-54
 Sequence 54; Application US/08232539D
 Patent No. 5965709
 GENERAL INFORMATION:
 APPLICANT: Prest, Leonard G.
 ATTORNEY/AGENT INFORMATION:
 ADDRESS: Genetech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPatin (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,539D
 FILING DATE: 21-Apr-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/178583
 FILING DATE: 07-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/744768
 FILING DATE: 14-AUG-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39 044
 REFERENCE/DOCKET NUMBER: P0718P3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 INFORMATION FOR SEQ ID NO: 54
 SEQUENCE CHARACTERISTICS:

; LENGTH: 106 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-232-539D-54

Query Match 29.0%; Score 538; DB 2; Length 106;
 Best Local Similarity 98.1%; Pred. No. 1.e-44;
 Matches 102; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 129 GVSAYLRSRSPSPFDLIRKSPPTICLVVLDAPSCKTQNLTWSRASGKPVNHSRKKEKORN 188
 Db 1 GVSAYLRSRSPSPFDLIRKSPPTICLVVLDAPSCKTQNLTWSRASGKPVNHSRKKEKORN 60

Qy 189 GTLTIVTSTLPGTRDIEGETYQCRVTHPHLPALMRSTKLPG 232
 Db 61 GTLTIVTSTLPGTRDIEGETYQCRVTHPHLPALMRSTKLPG 104

RESULT 12
 US-09-828-995B-38
 Sequence 38; Application US/09828995B
 Patent No. 6703360
 GENERAL INFORMATION:
 APPLICANT: Heska Corporation
 ATTORNEY/AGENT INFORMATION:
 Tang, Liang A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE IL-13
 FILE REFERENCE: AL-7
 CURRENT APPLICATION NUMBER: US/09/828,995B
 CURRENT FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 60/195,874
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: 60/195,659
 PRIOR FILING DATE: 2000-04-07
 NUMBER OF SEQ ID NOS: 104
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 38
 LENGTH: 352

Query Match 28.0%; Score 520.5; DB 4;
 Best Local Similarity 36.4%; Pred. No. 3.e-42;
 Matches 129; Conservative 58; Mismatches 138; Indels 29; Gaps 12;

Qy 5 HHHHHTSLIPPSGPVTTIPTVKLPHSSCDPRGDAHSTIOLCLVSGFSPAKVHVTWLYDG 64
 Db 10 HWGNGLSLFVSSAATSTAPSVPFLASCSTG---STVALACLVSGFPEPVWSNSSS 66

Qy 65 -QEAEMLPPYTTRKREGGOTSEQUESEVNITOGOMMSSNTYTCVHKENG-----IPE 116
 Db 67 LSGVHTTPSVL---QSSGLYLSLSTVPPSSRW-PSSETFTCNVHPASNTKVDKPVPK 121

Qy 117 DSSRKCADSNP---RGVSYAYLRSPSPPDLF-IRKSPTITCLVLDAPSCKTQNLTWSR 170
 Db 122 ESTRCICISPVPVPESSIGGPSPVFFPPKPKDILRTRPBTICVVLGLGREDPVQISWF- 180

Qy 171 ASGKPVNHS-TRKEEKQRNGTLTVSTLPGTRDIEGETYQCRVTHPHLPALMRSTKL 22.9
 Db 181 VDGKEVHTAKTQPQQQNSTYRVSVLPIEHDWLITGKEPKCRVNHIGLPSPIERTISK 240

Qy 230 LPGKRLAPEYMLPPSPEE-TGTTRTVCLIRGFYPSISVOWLNNEEDHTGHHTTR 287
 Db 241 ARGQAHQPSVYVLPSPKELSSDDTVTLCLIQFPPBIDVEQNSNGOPEPESKYHTA 300

Qy 288 PQKDGTDPFELFLYRMLVYKSTWEKGNUVTCRYHEALPGSRTEKSLHYSAQ 341
 Db 301 PQDDE-DGSYFLYSLVDSRQGDFETCAWHEALQNYT-DLSLHSPG 351

RESULT 13
 US-09-828-995B-11

Sequence 11, Application US/09828995B
 Patent No. 6703360
 GENERAL INFORMATION:
 APPLICANT: Heska Corporation
 APPLICANT: Tang, Liang A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE II-13 R
 CURRENT APPLICATION NUMBER: US/09/828,995B
 CURRENT FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 60/195,874
 PRIOR FILING DATE: 2000-04-07
 PRIORITY NUMBER: 60/195,874
 NUMBER OF SEQ ID NOS: 104
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 11
 LENGTH: 470
 TYPE: PRT
 ORGANISM: Canis familiaris
 US-09-828-995B-11

Query Match 27.6%; Score 513; DB 4; Length 468;
 Best Local Similarity 36.4%; Pred. No. 2..8e-4;
 Matches 124; Conservative 58; Mismatches 121; Indels 38; Gaps 14;

Qy 23 PTVKLFHSSCDPGDASTIQLCLVSGFSPAKVHTW---LVDGEAENILFPYTRPK 78
 Db 143 PSVFLPLAPSCG---STSGSTVALACLVSGYFPEPVTVWSNSGLTSG---WHTFSPSVL---194
 Qy 79 REGQQTSIQLQEVNITQQMSNTYCHVRKNS-----IPEDSRKADSNP---127
 Db 195 -QSSGLHSLSMNTVPPSSR-W-SETETCNVTHPASNTKVDEVFNEC--RCIDTPPPVVP 250
 Qy 128 ---RGVAYSLRSRSPFDLF-IRKSPTITCLVYDLPKGTVNLTWASGRPVNH-TRK 182
 Db 251 EPLGGPSVLIFPPKPD-LRITRTPETCVVLDLGREDPEQVQISWF-VDGKEVHTAKTQS 309
 Qy 183 EERKONGTILTVTSTLPCTRDVEGETYQCRVTHPHPRALMRSTMLPGERLAPVYML 242
 Db 310 REQQNGTYRVSVLP-EHQDWITGKEKCRYNHDDSPERTISARGRAHKPSVYVL 369

Query Match 28.0%; Score 519.5; DB 4; Length 470;
 Best Local Similarity 36.4%; Pred. No. 6.5e-12;
 Matches 130; Conservative 58; Mismatches 134; Indels 35; Gaps 13;

Qy 5 HHHTLSELPEGVTTIPPTVKLFHSSCDPREGDASTIQLCLVSGFSPAKVHTW---60
 Db 128 HWENGTSFLVFSSASTTAPSVPFLAPSCGSTSG---STVALACLVSGYFPEPVTVWSNSGS 184
 Qy 61 LVQGQEANLFPTRPKREGGTFSTIQLQGWMSSNTYCHVRKNS-----113
 Db 185 LTSG---VHTPPSVL---QSSGLYLSLSSVTUPSSR-PSETETCNVWVBPASNTKVDP 236
 Qy 114 IFDSSRKADSNP---RGVAYSLRSRSPFDLF-IRKSPTITCLVYDLPKGTVNL 167
 Db 237 VPKESTCRISCPVPPESLGGSVFIPPKPFDILTRPEITCVLDLGREDPEVQIS 296
 Qy 168 WSRASGKEVNH-STRKEKQRGNTLTIVTSTLPVGTRDWIEGETYQCRVTHPHPRALMS 226
 Db 297 WF-VDGEKEVHTAKTQPQQFNSTYRVSVLPIEHQOWLTKREFCRVNLGLPSPIER 355
 Qy 227 TTKLPGKBLAEPVYMLPSSPEE-TCTGTPTTCLIGFYPSEIISIOWLNNEEHTGHT 284
 Db 356 ISRKQGAHQPSVYLPSPSKPLSSSDTPTCLIDFPPDIDEWQSQCPEPESKYH 415
 Qy 285 TTRQDKHGTDPSFPLYSMLVNSLMEKGNLVTCRPHALPGSRTLESLHYSAG 341
 Db 416 TTAQQLD-EQSYEFLSKLSYDKSRMQGDTFTCAWHEALQHYT-DLSLHSPG 469

RESULT 15
 US-08-646-981-16
 Sequence 16, Application US/08646981
 Patent No. 5852183
 GENERAL INFORMATION:
 APPLICANT: MAEDA, HIROAKI
 APPLICANT: EDA, YASUTAKI
 APPLICANT: KIMACHI, KAZUHIKO
 APPLICANT: ONO, YOICHI
 APPLICANT: TOKUYOSHI, SACHIO
 TITLE OF INVENTION: DOG MOUSE HETEROHYBRIDOMA AND GENE
 TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
 TITLE OF INVENTION: IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASSCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22044-0747
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/646,981.
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: WEINER, MARC S
 REGISTRATION NUMBER: 32,181
 REFERENCE/DOCKET NUMBER: 1488-106
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 334 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-646-981-16

RESULT 14
 US-09-828-995B-5
 Sequence 5, Application US/09828995B
 Patent No. 6703360
 GENERAL INFORMATION:
 APPLICANT: Heska Corporation
 APPLICANT: McCall, Catherine A.
 APPLICANT: Tang, Liang A.
 TITLE OF INVENTION: COMPOSITIONS AND METHODS RELATED TO CANINE IgG AND CANINE II-13 R
 FILE REFERENCE: AL-7
 CURRENT APPLICATION NUMBER: US/09/828,995B
 CURRENT FILING DATE: 2001-04-09
 PRIOR APPLICATION NUMBER: 60/195,874
 PRIOR FILING DATE: 2000-04-07
 PRIOR APPLICATION NUMBER: 60/195,659
 PRIOR FILING DATE: 2000-04-07
 NUMBER OF SEQ ID NOS: 104
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 5
 LENGTH: 468
 TYPE: PRT
 ORGANISM: Canis familiaris

Query Match 27.6%; Score 512; DB 2; Length 334;
 Best Local Similarity 35.9%; Pred. No. 2.1e-41;
 Matches 113; Conservative 60; Mismatches 122; Indels 38; Gaps 12;

Qy 23 PTVKLPHSSCDPRGDAHSTIOLICLVSFGSPAKVHYTW---LVDGQBAENLFPYTRPK 78
 Db 5 PSVPLDPSCG--SISGGTVALAACLVSIFPEPSTVSWNSGSLTSG-----VHFFPSD 55

Qy 79 REGQQTFSLOSEVNITQGOMMSNTYTCVHKH-----NGSIEFE--DSSRK 121

Db 56 LQSSGLYSSMTPVSPSRW-SSEETETCNVAHBAKTMVKDVKPVKRENGRIVRPPDCPKC 114

Qy 122 CADENPRGYSAYLSRSPSPD-LIRKSPITCLUVVLDAPSKGTVNLTSWSASGKPVNHS- 179

Db 115 PAPEMLGGSSVPFLPPPKXDKDTLIARTBEVTCVVDLGPEDPEVQ1SWF-VDGKQKQTAK 173

Qy 180 TRKEBKQNGTLTVTSPVGTRDWWIGETBYQCRVTHPHPHALMRSTKLGKRLAPEV 239

Db 174 TQPSEEQNTGTYRVVSVPIGHODWLKQKQFTCKVANKALPPIERTISKARGQAHQPSV 233

Qy 240 YMPPPSPEB-TGTTRTVCLIRGFYPSBISYOWLENNEEDHGHHTTRPQDHGTDPSE 298

Db 234 YVLPPSREELSKNSVSLCLIODEFPPLDVQSNGQQEPSSKVRTPPQLDE--DGSY 291

Qy 299 FLYSRMLVINKSIWEKGNIYTCRVYHEALPGSRLEKSHYSAG 341

Db 292 FLYSKLSDVKSRSORGDFICAVHEALTHNHT-QKSLSHSPG 333

Search completed: November 14, 2004, 15:03:00
 Job time : 40 secs

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OM protein - protein search, using sw model

Run on: November 14, 2004, 15:01:45 ; Search time 144 Seconds

(without alignments)
840,320 Million cell updates/sec

Title: US-09-401-636-8

Perfect score: 1856

Sequence score: 1 EFPHHHHTLSSLPESGPVTLI.....HEALPGSRTEKSLHYSGN 342

Scoring table: BLOSUM62

gapop 10.0 / Gapext 0.5

Searched: 1568699 seqs, 353819137 residues

Total number of hits satisfying chosen parameters:

1568699

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA.*

- 1: /cn2_6/ptodata/1/pubaa/US07_PUBCOMB.pep:*
- 2: /cn2_6/ptodata/1/pubaa/PCT_NEW_PUB.pep:*
- 3: /cn2_6/ptodata/1/pubaa/US06_NEW_PUB.pep:*
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- 10: /cn2_6/ptodata/1/pubaa/US09_PUBCOMB.DEP:*
- 11: /cn2_6/ptodata/1/pubaa/US09C_PUBCOMB.DEP:*
- 12: /cn2_6/ptodata/1/pubaa/US09_NEW_PUB.pep:*
- 13: /cn2_6/ptodata/1/pubaa/US10A_PUBCOMB.DEP:*
- 14: /cn2_6/ptodata/1/pubaa/US10B_PUBCOMB.DEP:*
- 15: /cn2_6/ptodata/1/pubaa/US10C_PUBCOMB.DEP:*
- 16: /cn2_6/ptodata/1/pubaa/US10D_PUBCOMB.DEP:*
- 17: /cn2_6/ptodata/1/pubaa/US10_NEW_PUB.pep:*
- 18: /cn2_6/ptodata/1/pubaa/US11_NEW_PUB.pep:*
- 19: /cn2_6/ptodata/1/pubaa/US60_NEW_PUB.pep:*
- 20: /cn2_6/ptodata/1/pubaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query %

Match Length DB ID

Description

Result No.	Score	Query %	Match Length	DB ID	Description
1	1856	100.0	342	9	US-09-401-636-8
2	1856	100.0	342	14	US-10-433-915-14
3	1856	100.0	342	15	US-10-673-594-8
4	1786	96.2	338	15	US-10-438-794-6
5	1786	96.2	338	15	US-10-433-915-6
6	1786	96.2	347	15	US-10-438-794-14
7	1786	96.2	347	15	US-10-433-915-14
8	1772	95.5	557	15	US-10-438-794-12
9	1772	95.5	557	15	US-10-433-794-16
10	1772	95.5	557	15	US-10-433-911-12
11	1772	95.5	557	15	US-10-433-915-16
12	1772	95.5	566	15	US-10-438-794-18
13	1772	95.5	566	15	US-10-438-794-18

OTHER INFORMATION: Synthetically generated proteins

SEQ ID NO 8

LENGTH: 342

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

RESULT 1
US-09-401-636-8
; Sequence 8, Application US/09401636
; Patient No. US20011038843A1
; GENERAL INFORMATION:
; APPLICANT: Hellman, Lars T.
; TITLE OF INVENTION: ENHANCED VACCINES
; FILE REFERENCE: 10223/005001
; CURRENT APPLICATION NUMBER: US/09-401-636
; CURRENT FILING DATE: 1999-09-22
; PRIOR APPLICATION NUMBER: US 60/116,652
; PRIOR FILING DATE: 1998-11-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 342
; OTHER INFORMATION: Synthetically generated proteins
US-09-401-636-8

ALIGNMENTS

Query Match 100.0%; Score 1856; DB 9; Length 342;
Best Local Similarity 100.0%; Pred. No. 1.5e-139;
Matches 342; Conservativeness 0; Mismatches 0; Gaps 0;

Qy	1	EFPHHHHTLSSLPESGPVTIIPPPVKEFHSSCDPRGDAHSTIQCLYSGFSPAKVHYTW
Db	1	EFPHHHHTLSSLPESGPVTIIPPPVKEFHSSCDPRGDAHSTIQCLYSGFSPAKVHYTW
Qy	61	LVDGQEAEFLFPYTPRKREGGQTISLQSEVNITQGQMSNTYTCYHGNGSFEDSSR
Db	61	LVDGQEAEFLFPYTPRKREGGQTISLQSEVNITQGQMSNTYTCYHGNGSFEDSSR
Qy	121	KCADSNPGRGAYSLSRPSPDFLRKSPTTCLVYDLAPSGBTNTLWSRASGPVNHT

RESULT 2

Sequence 8, Application US/10176664

Publication No. US20030031663A1

APPLICANT: Hellman, Lars T.

TITLE OF INVENTION: ENHANCED VACCINES

CURRENT APPLICATION NUMBER: US/10/673,594

CURRENT FILING DATE: 2003-09-29

PRIOR APPLICATION NUMBER: US/09/401,616

PRIOR FILING DATE: 1999-09-22

PRIOR APPLICATION NUMBER: US 60/106,652

PRIOR FILING DATE: 1998-11-02

NUMBER OF SEQ ID NOS: 11

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 8

LENGTH: 342

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetically generated proteins

US-10-673-594-8

Query Match 100.0%; Score 1856; DB 15; Length 342;

Best Local Similarity 100.0%; Pred. No. 1.5e-139;

Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 EFHHHHHTLSLPSGPVTTIIPPTVKEFHSSCDPRGDAHSTIQLCLVSGSFSPAKVTW 60

Db 1 EFHHHHHTLSLPSGPVTTIIPPTVKEFHSSCDPRGDAHSTIQLCLVSGSFSPAKVTW 60

Qy 61 LDGQEAENLFPTTTRPKEGGTFSLOSEVNITQGMMSNTYTCVKINGSIFEDSSR 120

Db 61 LDGQEAENLFPTTTRPKEGGTFSLOSEVNITQGMMSNTYTCVKINGSIFEDSSR 120

Qy 121 KCADSNPREGVASYLSRSPFDLIRKSPTITCLVVDLAPSCKTVNLTSRASGKPTNHST 180

Db 121 KCADSNPREGVASYLSRSPFDLIRKSPTITCLVVDLAPSCKTVNLTSRASGKPTNHST 180

Qy 181 RKEEKFQRNGLTTLVSTLPGTTRDVGTYOCRVTHPLPRLMRSTTKLPGRKLAPEVY 240

Db 181 RKEEKFQRNGLTTLVSTLPGTTRDVGTYOCRVTHPLPRLMRSTTKLPGRKLAPEVY 240

Qy 241 MLPPSPBETGTTRTVTCIIRGFYPSSESVQMLFNNEBDHTGHHTTPFQDKDHGTDPSFFL 300

Db 241 MLPPSPBETGTTRTVTCIIRGFYPSSESVQMLFNNEBDHTGHHTTPFQDKDHGTDPSFFL 300

Qy 301 YSRMLVNSIWEKGNLVTCRVHEALPSRTELEKSLIYSAGN 342

Db 301 YSRMLVNSIWEKGNLVTCRVHEALPSRTELEKSLIYSAGN 342

RESULT 4

Sequence 8, Application US/10176664

Publication No. US20030031663A1

GENERAL INFORMATION:

APPLICANT: LUNIGREN, Mats

ATTORNEY: FUENTES, Alexis

APPLICANT: MAGNUSSON, Ann-Christian

TITLE OF INVENTION: Chimeric IGE Polypeptides and Host Cells

FILE REFERENCE: 10223-017001

CURRENT APPLICATION NUMBER: US 10/438,794

CURRENT FILING DATE: 2003-05-15

PRIOR APPLICATION NUMBER: US 60/382,552

NUMBER OF SEQ ID NOS: 20

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 6

LENGTH: 338

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Synthetic polypeptide designated OSO

US-10-438-794-6

Query Match 96.2%; Score 1786; DB 15; Length 338;

RESULT 3

Sequence 8, Application US/10673594

Publication No. US20040076625A1

GENERAL INFORMATION:

PRIOR APPLICATION NUMBER: 60/408, 648
 PRIORITY FILING DATE: 2002-09-05
 SEQ ID NO: 24
 SOFTWARE: Fast-SEQ for Windows Version 4.0
 LENGTH: 347
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE: OTHER INFORMATION: chimeric polypeptide
 US-10-453-915-14

Query Match Score 96.2%; Length 1786; DB 15; Length 347;
 Best Local Similarity 99.4%; Pred. No. 5..9e-134;
 Matches 334; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

Qy 9 TLSLPESGPTVIIPTPVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEA 68
 Db 3 TLSLPESGPTVIIPTPVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEA 62

Qy 69 NLFPYTTREKREGQQTFSLOSEVNITQGQMSNTYTCVHKNGSIEDDSRKCADSNPR 128
 Db 63 NLFPYTTREKREGQQTFSLOSEVNITQGQMSNTYTCVHKNGSIEDDSRKCADSNPR 122

RESULT 9
 US-10-438-794-16
 ; Sequence 16, Application US/10438794
 ; GENERAL INFORMATION:
 ; PUBLICATION NO. US 20040038395A1
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-794
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 16
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated OSOSO
 US-10-438-794-16

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGRAHSTIQLCLVSGFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGRAHSTIQLCLVSGFPAKVHTWLVDGQAEIN 284

RESULT 8
 US-10-438-794-12
 ; Sequence 12, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 12
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-12

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 7
 US-10-438-794-11
 ; Sequence 11, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 11
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-11

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 6
 US-10-438-794-10
 ; Sequence 10, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 10
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-10

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 5
 US-10-438-794-9
 ; Sequence 9, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 9
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-9

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 4
 US-10-438-794-8
 ; Sequence 8, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 8
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-8

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 3
 US-10-438-794-7
 ; Sequence 7, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 7
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-7

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 2
 US-10-438-794-6
 ; Sequence 6, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 6
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-6

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 1
 US-10-438-794-5
 ; Sequence 5, Application US/10438794
 ; Publication No. US 20040038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDREN, Mats
 ; FVENTES, Alexis
 ; MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; CURRENT APPLICATION NUMBER: US 10/438-07001
 ; CURRENT FILING DATE: 2003-05-15
 ; PRIOR APPLICATION NUMBER: US 60/382, 552
 ; PRIOR FILING DATE: 2002-05-21
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 5
 ; LENGTH: 557
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic polypeptide designated modOSOSO
 US-10-438-794-5

Query Match Score 95.5%; Length 1772; DB 15;
 Best Local Similarity 98.5%; Pred. No. 1..4e-122;
 Matches 328; Conservative 2; Mismatches 0;
 Indels 0; Gaps 0;

Qy 10 LSILPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQEAEN 69
 Db 225 IDIPESGPVIIIPPTVKLFHSSCDPRGDAAHSTIQCLVLSCFSPAKVHTWLVDGQAEIN 284

RESULT 10
US-10-43-915-12
Sequence 12, Application US/10453915
Publication No. US20040054146A1
GENERAL INFORMATION:
APPLICANT: Hellman, Lars T.
APPLICANT: Jansson, Stefan
APPLICANT: Jansson, Asa
TITLE OF INVENTION: Allergy Vaccines
FILE REFERENCE: 10223-008001
CURRENT APPLICATION NUMBER: US/10/453, 915
PRIOR APPLICATION NUMBER: 60/1408, 648
PRIOR FILING DATE: 2003-06-02
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO: 12
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: chimeric polypeptide
US-10-453-915-12

Query Match 95.5%; Score 1772; DB 15; Length 557;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LSLPESGPVIIIPPTVKLFHSSCDPRGAHSTIOLCLVSGFSPAKVHTWLVDGQEAEEN 69
Db 225 IDIPSGPVIIIPPTVKLFHSSCDPRGAHSTIOLCLVSGFSPAKVHTWLVDGQEAEEN 284

Qy 70 LFPTTRPKREGQTSLOSEVNITQGMSSNTYCHVKGNSIFPESRKCADSNPRG 129
Db 285 LFPTTRPKREGQTSLOSEVNITQGMSSNTYCHVKGNSIFEDSSRKCADSNPRG 344

Qy 130 VSAYLRSRSPFDLFIKSPTITCLVVDLAPSKGTVNLWASGKPNHSTRKEEKQNG 189
Db 345 VSAYLRSRSPFDLFIKSPTITCLVVDLAPSKGTVNLWASGKPNHSTRKEEKQNG 404

Qy 190 TLTVTSTLPGRDWTIGEYQCRVTHPLPRAIMRSTKLPGKRLAEGVMLPPSPEET 249
Db 405 TLTVTSTLPGRDWTIGEYQCRVTHPLPRAIMRSTASPGKRLAEGVMLPPSPEET 464

Qy 250 GTTRTVTCLJRGFYPESEISVQWLNNEEDHTGHHTTRPKDHGTDPSFLYTSRMLVNRK 309
Db 465 GTTRTVTCLJRGFYPESEISVQWLNNEEDHTGHHTTRPKDHGTDPSFLYTSRMLVNRK 524

Qy 310 IWEKGNLTCRVVHAPGSRTLEKSHYSAGN 342
Db 525 IWEKGNLTCRVVHAPGSRTLEKSHYSAGN 557

RESULT 12
US-10-43-915-10
Sequence 10, Application US/10438794
Publication No. US20040039395A1
GENERAL INFORMATION:
APPLICANT: FUENTES, Alexis
APPLICANT: MAGNUSSON, Ann-Christin
TITLE OF INVENTION: Chimeric IGE Polypeptides and Host Cells
FILE REFERENCE: 10223-017001
CURRENT APPLICATION NUMBER: US/10/438,794
PRIORITY DATE: 2003-05-15
PRIORITY APPLICATION NUMBER: US 60/382,552
PRIORITY FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 10
LENGTH: 566
TYPE: PRT
ORGANISM: Artificial Sequence
OTHER INFORMATION: Synthetic polypeptide designated modososo-H
US-10-43-915-10

Query Match 95.5%; Score 1772; DB 15; Length 566;
Best Local Similarity 98.5%; Pred. No. 1.4e-132;
Matches 328; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LSJPESGPVIIIPPTVKLFHSSCDPRGAHSTIOLCLVSGFSPAKVHTWLVDGQEAEEN 69
Db 225 IDIPSGPVIIIPPTVKLFHSSCDPRGAHSTIOLCLVSGFSPAKVHTWLVDGQEAEEN 284

Qy 70 LFPTTRPKREGQTSLOSEVNITQGMSSNTYCHVKGNSIFPESRKCADSNPRG 129
Db 285 LFPTTRPKREGQTSLOSEVNITQGMSSNTYCHVKGNSIFEDSSRKCADSNPRG 344

Qy 130 VSAYLRSRSPFDLFIKSPTITCLVVDLAPSKGTVNLWASGKPNHSTRKEEKQNG 189
Db 345 VSAYLRSRSPFDLFIKSPTITCLVVDLAPSKGTVNLWASGKPNHSTRKEEKQNG 404

RESULT 13
 US-10-438-794-18
 ; Sequence 18 , Application US/10438794
 ; Publication No. US2004038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: LUNDGREEN, Mats
 ; FUENTES, Alexis
 ; ATTORNEY: MAGNUSSON, Ann-Christin
 ; TITLE OF INVENTION: Chimeric IgE Polypeptides and Host Cells
 ; FILE REFERENCE: 1023-017001
 ; CURRENT APPLICATION NUMBER: US 10/438,794
 ; PRIORITY FILING DATE: 2003-05-15
 ; PRIORITY APPLICATION NUMBER: US 60/382,552
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 18
 ; LENGTH: 566
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chimeric polypeptide
 ; US-10-453-915-10

Query Match 95.5%; Score 1772; DB 15; Length 566;
 Best Local Similarity 98.5%; Pred. No. 1.4e-132;
 Matches 328; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LSLPESGPVTTIPPTVKLFHSSCDPRAHSTIQCLVLVSGETSPAKVHVTWLVDCQAEN 69
 Db 225 IDIPESGPVTTIPPTVKLFHSSCDPRAHSTIQCLVLVSGETSPAKVHVTWLVDCQAEN 284

Qy 70 LFPTTTRPREGQTFLQSEVNITQGMSNTYCHVNGSIFEDSSRKCADSNPRG 129
 Db 285 LFPTTTRPREGQTFLQSEVNITQGMSNTYCHVNGSIFEDSSRKCADSNPRG 344

Qy 130 VSAYLSRSPSPFDLFIRESPTITCLVVDLAPSKGTYNLTWSRASGPVNHSTRKEKQRNG 189
 Db 345 VSAYLSRSPSPFDLFIRESPTITCLVVDLAPSKGTYNLTWSRASGPVNHSTRKEKQRNG 404

Qy 190 TLTVTSPLPVGRDWTIGETYQCRVTHPHLRAPEYMLPPSPEET 249
 Db 405 TLTVTSPLPVGRDWTIGETYQCRVTHPHLRAPEYMLPPSPEET 464

Qy 250 GTTRTVTLIRGFYPSLSVQNLNFNEEDHTGHHTTRPQDHGTDPSFLYSRMLVNRK 309
 Db 525 GTTRTVTLIRGFYPSLSVQNLNFNEEDHTGHHTTRPQDHGTDPSFLYSRMLVNRK 524

Query Match 95.5%; Score 1772; DB 15; Length 566;
 Best Local Similarity 98.5%; Pred. No. 1.4e-132;
 Matches 328; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 10 LSLPESGPVTTIPPTVKLFHSSCDPRAHSTIQCLVLVSGETSPAKVHVTWLVDCQAEN 69
 Db 225 IDIPESGPVTTIPPTVKLFHSSCDPRAHSTIQCLVLVSGETSPAKVHVTWLVDCQAEN 284

Qy 70 LFPTTTRPREGQTFLQSEVNITQGMSNTYCHVNGSIFEDSSRKCADSNPRG 129
 Db 285 LFPTTTRPREGQTFLQSEVNITQGMSNTYCHVNGSIFEDSSRKCADSNPRG 344

Qy 130 VSAYLSRSPSPFDLFIRESPTITCLVVDLAPSKGTYNLTWSRASGPVNHSTRKEKQRNG 189
 Db 345 VSAYLSRSPSPFDLFIRESPTITCLVVDLAPSKGTYNLTWSRASGPVNHSTRKEKQRNG 557

RESULT 15
 US-10-453-915-18
 ; Sequence 18 , Application US/10453915
 ; Publication No. US2004038395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hellman, Lars T.
 ; ATTORNEY: Stefan
 ; APPLICANT: Jansson, Asa
 ; TITLE OF INVENTION: Allergy Vaccines
 ; FILE REFERENCE: 10223-008001
 ; CURRENT APPLICATION NUMBER: US/10453,915
 ; CURRENT FILING DATE: 2003-06-02
 ; PRIOR APPLICATION NUMBER: 60/408,648
 ; PRIOR FILING DATE: 2002-09-05
 ; NUMBER OF SEQ ID NOS: 24
 ; SOFTWARE: Fast-SEQ for Windows Version 4.0
 ; SEQ ID NO: 18
 ; LENGTH: 566
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: chimeric polypeptide
 ; US-10-453-915-18

Query Match 95.5%; Score 1772; DB 15; Length 566;
 Best Local Similarity 98.5%; Pred. No. 1.4e-132;

Matches	328:	Conservative	2;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	10	LSPSGPVIIIPPTVYLPHSSCDPRGDASHSTIQLCLVSGFPARVTWLVDGQEAEEN	69						
Db	225	IDIPSGPVIIIPPTVYLPHSSCDPRGDASHSTIQLCLVSGFPARVTWLVDGQEAEEN	69						
Qy	70	LFPYTRPREGQTFSLOSEVNITQGOMMSNTYTCVKGNSSFEDSSRKCADSNPRG	129						
Db	285	LFPYTRPREGQTFSLOSEVNITQGOMMSNTYTCVKGNSSFEDSSRKCADSNPRG	129						
Qy	130	VSAYLSRSPSPFDLTKSPITCLVVDAPIASKGTVNLTWSRASGKPYNHSTRKEEKONG	189						
Db	345	VSAYLSRSPSPFDLTKSPITCLVVDAPIASKGTVNLTWSRASGKPYNHSTRKEEKONG	189						
Qy	190	TLTVTSTLPVGTRWIEGETYCGRVTHPHLPRALMRSTKLCKRILAPEVYMLPPSPET	249						
Db	405	TLTVTSTLPVGTRWIEGETYCGRVTHPHLPRALMRSTASPKRILAPEVYMLPPSPET	464						
Qy	250	GTTRTVTCLIRGFYPSESVQMLFNNEEDHTGHHTTRPQDHGTDPSSFLYSRMLVNGS	309						
Db	465	GTTRTVTCLIRGFYPSESVQMLFNNEEDHTGHHTTRPQDHGTDPSSFLYSRMLVNGS	524						
Qy	310	IWERGNLIVTCRYTHEALCSRTELEKSLIYSAGN	342						
Db	525	IWERGNLIVTCRYTHEALCSRTELEKSLIYSAGN	557						

Search completed: November 14, 2004, 15:13:50
 Job time : 145 secs

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Copyright (c) 1993 - 2004 Compugen Ltd.	Ig mu chain C regi	30	453.5	24.4	473	1	MHHM
OM protein - protein search, using sw model	Ig mu chain C regi	31	450	24.2	457	2	S03961
Run on: November 14, 2004, 14:55:22 ; Search time 40 seconds (without alignments)	Ig gamma 4 chain C	32	447	24.1	277	2	A27162
Title: US-09-401-636-8	Ig gamma-3 chain C	33	447	24.1	377	2	A23511
Perfect score: 1856	Ig heavy chain V r	34	447	24.1	377	2	A60764
Sequence: 1 EFHHHHHHTLSEKSHYSAGN 342	Ig mu chain C regi	35	446.5	24.1	374	2	S69339
Scoring table: BLOSUM62	Ig gamma-1 chain	36	444	23.9	450	1	MHDG
Searched: Gapop 10.0 , Gapext 0.5	Ig gamma-1 chain C	37	443.5	23.9	322	2	PS0019
Total number of hits satisfying chosen parameters: 283416	Ig gamma-1 chain C	38	440	23.7	323	1	S31459
Minimum DB seq length: 0	Ig gamma chain C region	39	437.5	23.6	323	1	GHRB
Maximum DB seq length: 20000000000	Ig epsilon chain C region	40	437.5	23.6	444	2	PC4436
Post-processing: Minimum Match 0% Maximum Match 100%	C;Species: Homo sapiens (man)	41	436.5	23.5	326	2	PS0017
Listing first 45 summaries	C;Date: 31-Mar-1981 #sequence revision 13-Jun-1983 #text change 09-Jul-2004	42	429	23.1	470	2	S22080
Database : PIR_79;* 1: pi;r1;* 2: pi;r2;* 3: pi;r3;* 4: pi;r4;*	C;Accession: A22771; A23195; BHL214; A93491; A90824; A94419; B33933; S02438; A53116; C4 R;Flanagan, J.G.; Rabbits, T.H.	43	428	23.1	329	2	S00847
	EMBO J. 1, 655-660, 1982	44	428	23.1	549	2	S04845
	A;Title: The sequence of a human immunoglobulin epsilon heavy chain constant region gen	45	424.5	22.9	329	1	G2GP
	A;Reference number: A22771; MUID:84236029; PMID:6234164						
	A;Molecule type: DNA						
	A;Residues: 1-28 < PIA>						
	A;Cross-references: UNIPROT: P01854; GB:L00022; GB:J00227; GB:V00555; NID:g185055						
	R;Ueda, S.; Nakai, S.; Nishida, Y.; Hisajima, H.; Horijo, T.						
	EMBO J. 1, 1539-1546, 1982						
	A;Title: Long terminal repeat-like elements flank a human immunoglobulin epsilon pseudo						
	A;Reference number: A23195; MUID:84207910; PMID:632276						
	A;Accession: A23195						
	A;Molecule type: DNA						
	A;Residues: 2-128 < PBD>						
	A;Cross-references: GB:J00222; NID:g184755						
	R;Zhang, K.; Saxon, A.; Max, E.E.						
	J. Exp. Med. 176, 233-243, 1992						
	A;Title: Two unusual forms of human immunoglobulin E encoded by alternative RNA splicin						
	A;Reference number: PH1214; MUID:92308839; PMID:1613458						
	A;Molecule type: DNA						
	A;Cross-references: EMBL:X63693; GB:S38668; NID:932987						
	R;Seno, M.; Kurokawa, T.; Ono, Y.; Onda, H.; Sasada, R.; Iguchi, M.; Sug						
	Nucleic Acids Res. 11, 719-726, 1983						
	A;Title: Molecular cloning and nucleotide sequencing of human immunoglobulin epsilon ch						
	A;Reference number: A93491; MUID:8316897; PMID:6300763						
	A;Accession: A93491						
	A;Molecule type: mRNA						
	A;Residues: 1-428 < SEN>						
	A;Cross-references: GB:L00022; GB:J00227; GB:V00555; NID:9185035						
	R;Max, E.E.; Battye, J.; Ney, R.; Kirsch, I.R.; Leder, P.						
	Cell 29, 691-699, 1982						
	A;Title: Duplication and deletion in the human immunoglobulin epsilon genes.						
	A;Reference number: A90824; MUID:83001945; PMID:6288268						
	A;Accession: A90824						
	A;Molecule type: DNA						
	A;Residues: 1-358 'L' 360-428 <MX>						
	A;Cross-references: GB:J00222; NID:g184755						
	A;Note: this sequence difference may be due to polymorphism						
	R;Bennich, H.H.; Johansson, S.G.O.; Von Bahr-Lindstrom, H.						
	In Immediate Hypersensitivity: Modern Concepts and Developments, Bach, M.K., ed., pp.1-1.						
	A;Reference number: A94418						
	A;Accession: A94418						
	A;Molecule type: protein						

A;Residues: 'GAWL', 6; 'X', 8-16; 'B', 18-43; 'B', 45-52, 55-92, 95-97; 'B', 99-121; 'B', 123; 'L', 12
A;Experimental source: myeloma protein Nd
R;Krenten, J. H.; Molgaard, H.V.; Houghton, M.; Derbyshire, R.B.; Viney, J.; Bell, L.O.; C
Proc. Natl. Acad. Sci. U.S.A. 79, 6651-6655, 1982
A;Title: Cloning and sequence determination of the gene for the human immunoglobulin epsilon
A;Reference number: A93933; MUID: 6815656
A;Accession: B9333
A;Molecule type: mRNA
A;Residues: 1-40; 68-114; 427-428 <KEN>
A;Cross-references: GB:L00022; NID:9185035
R;Ikeyama, S.
FEBS Lett. 224, 306-310, 1987
A;Reference number: S02438; MUID:88083554; PMID:3121387
A;Accession: S02438
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 98-352 <IKE>
R;Zhang, K.; Max, E. E.; Cheah, H.K.; Saxon, A.
J. Biol. Chem. 259, 456-466, 1984
A;Title: Complex alternative RNA splicing of epsilon-immunoglobulin transcripts produces
A;Reference number: A53116; MUID: 94103254; PMID:8276835
A;Accession: A53116
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 320-428 <ZH2>
A;Experimental source: myeloma U266-derived cell line AF-10
A;Note: sequence extracted from NCBI backbone (NCBIN:141701, NCBIP:141702)
R;Hellman, L.
Eur. J. Immunol. 23, 159-167, 1993
A;Title: Characterization of four novel epsilon chain mRNA and a comparative analysis of
A;Reference number: A46536; MUID: 93122085; PMID:8419166
A;Accession: C46536
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 382-426 <HEL>
A;Cross-references: GB:S55273; NID:9263166; PID:9263167
A;Experimental source: B cell myeloma U-266
A;Accession: D46536
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 382-391 <HE2>
A;Cross-references: GB:S55276; NID:9263167; PID:9263169
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIN:125299)
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 401-428 <HE3>
A;Cross-references: GB:S553437; NID:9263162; PID:9263163
A;Experimental source: B cell myeloma U-266
A;Note: sequence extracted from NCBI backbone (NCBIN:123483)
C;Genetics:
A;Gene: GDB:1GHE
A;Cross-references: GDB:119335; OMIM:147180
A;Intron position: 14q22.3-14q32.3-33
A;Intron: 1/1; 104/1; 211/1; 319/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain) disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobu
E:122-87/Domain: immunoglobulin homology <IM1>
E:128-301/Domain: immunoglobulin homology <IM3>
E:133-407/Domain: immunoglobulin homology <IM4>
E:145-105-29-55, 135-193, 239-299, 345-405/Disulfide bonds: #status predicted
E:21, 49, 99-146, 252-275/Binding site: carbohydrate (Asn) (covalent) #status experimental
E:21, 209/Disulfide bonds: interchain (to light chain) #status predicted
Query Match 56.0%; Score 1038.5; DB 1; Length 428;
Best Local Similarity 62.4%; Pred. No. 7.e-70;

Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;
Qy 22 PPTVLFHSSCDPFDKDTIQLCLVSGFSPAKVHTWLVDGOEAENLFPYTRKEREG 81
Db 111 PPTVKLQSSCDGGHPPTIQLCLVSGYFGTINTWLEDQVMD-VDLSTASTQE 168
Qy 82 QTFSLQSEVNITQGOMMSNTYTCVKGNSIFEDSSRKCADSNPRGVSAYLRSRSPFD 141
Db 169 ELASTQELTSQKHWLSDRTYCQVTTQGGTFFEDSTKKCASNPRGVSAYLRSRSPFD 228
Qy 142 LFIRKSPSPITCLVYDIAPSKGTVNLTMWSRASGKPVNHSRKEKQRNGTLTVTSLPGT 201
Db 229 LFIRKSPSPITCLVYDIAPSKGTVNLTMWSRASGKPVNHSRKEKQRNGTLTVTSLPGT 288
Qy 202 RDWIEGETYQCRYTHPHILPRLMRSTKLPGKRLAPAVYMLPPSPETGT-TRTVYCL 259
Db 289 RDWIEGETYQCRYTHPHILPRLMRSTKLTKTSGRRAAPPVYAF ATPEPGSRDKRTLA CLI 347
Qy 260 RGFPYSEISVQWLFNNEEDHTGHHTTPQDHGTDSFLFYSRMLVNLNSWEKGNLVTC 319
Db 348 QNFMPEDISVQWLNEQVLDARHSTQPRTKGS-GFVFESRLEVTRAWEQKDFIFIC 405
Qy 320 RYTHEALPGSRTLEKSLHYSG 341
Db 406 RAYEAAASPSQTQRAYSVNPG 427

RESULT 2
I3648
IG epsilon-chain - chimpanzee (fragment)
C;Species: Pan troglodytes (chimpanzee)
C;Date: 04-Oct-1996 #sequence_revision 04-Oct-1996 #text_change 21-Jan-2000
C;Accession: I36948
R;Sekoyama, Y.; Hong, K.
Proc. Natl. Acad. Sci. U.S.A. 84, 1080-1084, 1987
A;Title: Nucleotide sequences of immunoglobulin epsilon genes of chimpanzee and orangutan
A;Reference number: I36948; MUID:87147196; PMID:3103123
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-426 <RES>
A;Cross-references: GB:MI5398; NID:9176797; PID:AAA35416.1; PID:9176798
C;Genetics:
A;Intron: 103/1; 209/1; 317/1
C;Superfamily: immunoglobulin C region; immunoglobulin homology <IMM>
F:336-405/Domain: immunoglobulin homology <IMM>
Query Match 55.2%; Score 1024.5; DB 2; Length 426;
Matches 198; Conservative 42; Mismatches 7; Indels 7; Gaps 4;
Qy 23 PTVLFHSSCDPFDKDTIQLCLVSGFSPAKVHTWLVDGOEAENLFPYTRKEGG 82
Db 110 PTVVKLQSSCDGGHPPTIQLCLVSGYFGTINTWLEDQVMD-VDLSTASTAQEG 167
Qy 83 QTFSLQSEVNITQGOMMSNTYTCVKGNSIFEDSSRKCADSNPRGVSAYLRSRSPFD 142
Db 168 ELASTQELTSQKHWLSDRTYCQVTTQGGTFFEDSTKKCASNPRGVSAYLRSRSPFD 227
Qy 143 FIRKSPSPITCLVYDIAPSKGTVNLTMWSRASGKPVNHSRKEKQRNGTLTVTSLPGT 202
Db 228 FIRKSPSPITCLVYDIAPSKGTVNLTMWSRASGKPVNHSRKEQNRNGTLTVTSLPGT 287
Qy 203 DWIEGETYQCRYTHPHILPRLMRSTKLPGKRLAPAVYMLPPSPETGT-TRTVYCLIR 260
Db 288 DWIEGETYQCRYTHPHILPRLMRSTKLPGKRLAPAVYMLPPSPETGT-TRTVYCLIR 346
Qy 261 GFYSEISVQWLNEQVLDARHSTQPRTKGS-GFVFESRLEVTRAWEQKDFIFIC 320
Db 347 NFMPEDISVQWLNEQVLDARHSTQPRTKGS-GFVFESRLEVTRAWEQKDFIFIC 404
Qy 321 VVHEALPGSRTLEKSLHYSG 341

Db 405 AVHEAAASSPQTQRTVSYNPG 425

RESULT 3

BHRT

Ig epsilon chain C region - rat

C:Species: Rattus norvegicus (Norway rat)

C:Accession: A93442; A90937; A02143

R:Kellman, L.; Pettersson, U.; Zigstrom, A.; Karlsson, T.; Bennich, H.

DNA 1, 353-343, 1982

A:Title: Structure and domain of the heavy chain from rat immunoglobulin E.

A:Reference number: A93442; MUID:83064537; PMID:6292865

A:Accession: A93442

A:Residues: 1-429 <HEL>

A:Cross-references: UNIPROT:P01855

A:Experimental source: strain Lou/C/Wsl, immunocytoma IR2

R:Kindsvogel, W.R.; Reddy, E.P.; Moore, J.M.; Faust Jr., C.H.

DNA 1, 353-343, 1982

A:Title: A cloned cDNA probe for rat immunoglobulin epsilon chain: construction, i

A:Reference number: A90337; MUID:83182019; PMID:680340

A:Content: myeloma TR162

A:Accession: A90937

A:Residues: N, 168-07, 'L', 309-342 <KIN>

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

han) disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1α

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:18-80/Domain: immunoglobulin homology <IM1>

F:23-29/Domain: immunoglobulin homology <IM3>

F:27-39/Domain: immunoglobulin homology <IM4>

F:45,99,170,240,265,369,419/Binding site: carbohydrate (Asn) (covalent) #status predicte

Db 17 PVTIIPPTVKLEHSSCDPQGDAHTIQCLYGSFSPKAVHVTWLDGOEAENLFYPTTR 76

Db 97 PVNTKPTVDLHSSCDPNA-FHTIQLYCFFVGHIONDVSITWLMDDRKI-----YETH 150

QY 77 PK---REGQTFSHQSENNITQGMSSNTYCHVNGNSIFEDSSRKCADSNPRGYS 132

Db 151 AQNYLIKEBKLASTYQRNNTQOMWNEBESTFVKVTSQENYWAHRCSDEPROVIT 210

Db 133 YLSRPSPDFLFIKSPTTCLVNDAPSKGTYNLTWASGKPVNHSTRKEEKONGTLT 192

Db 211 YLIPSPDLYENTPKLTCVLDL-ESEENTIVTVWERKSISGQSRSKHHNAT 269

QY 193 VTSIIPVGTRDWIGETYQCRVTHPHPRALMRSTTLPKGELAPEVYMLPPSPEETGTT 252

Db 270 ITSLILPVADKWDIEEGGOCRVDHPHPKPIVRSITYXPGKESAPETYVFLPEEEKKDK 329

QY 253 RTVTCILRGFYPSSVQWLNNEEDHTFGHHTTRPOKDHTGTDPSFFLSRMVNSKWE 312

Db 330 RTLTCLQNFFPEDISVQWLDQSKLIPSPQHSITPLVYNGSQRFFFSSRLDVTAALWT 389

QY 313 KGNLVTCRVHEALPGSRTLEKSLHYSGN 342

Db 390 QTKOPTCRVTHEALREPRKLERTTSKSGN 419

A:Title: Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.

A:Reference number: A02144; MUID:811774; PMID:6818553

A:Residues: 1-388 <LIU>

A:Accession: A02144

A:Molecule type: mRNA

A:Residues: 1-388

C:Cross-references: UNIPROT:P06336; GB:J00476; PID:9194875; PID:938722

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

han) disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:1-44/Domain: immunoglobulin homology (fragment) <IM1>

F:186-254/Domain: immunoglobulin homology <IM2>

F:290-361/Domain: immunoglobulin homology <IM3>

F:290-361/Domain: immunoglobulin homology <IM4>

P:10,51,62,133,205,228,332,382/Binding site: carbohydrate (Asn) (covalent) #status pred

Query Match 40.5%; Score 751; DB 1; Length 388;

Best Local Similarity 44.8%; Pred. No. 1.7e-48;

Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;

QY 2 FHHHHHTLSPES----GPVTTIPPTVCLFHSSCDPQGDAHSHIQLLCLVSGFSPAKV 56

Db 40 FTCHVHPPSNESRILVTPVNITEPTLILLHSSCDPNA-FHSTIQLYCFIYGHILNDV 98

QY 57 HYTWLYDGQEENFLPYTTRPKREGQFTPSLOSEVNITIQGMSSNTYCHVRNGSIFE 116

Db 99 SVSWMNDRELTDTLAOTVLIKEGKLASTCSKLNITEQGMSSSTFTCKVTSQGVYDYL 157

QY 117 DSSRKADSNPNGVASYLSRSPFDIFIRKSPFTCLVWDLAPSGTYNNTWRSAGKPV 176

Db 158 AHTRCPDHERGVATYLISSLVLYONGAPKLTCVLVDLESK-NVNUVNWQEKKTSV 216

QY 177 NHSTRKBEKQKNGNTLTVTSTLPVGTRDWIGETYQCRVTHPHPRALMRSTTLPFKGRLLA 236

Db 217 SASQVNTKHANNTATITSILPVAIKDWEGYGQCVTWDHPFPVVISITKIFGQRSA 276

QY 237 PEVYMLPPSPREBTGTRTVCILRGFYPSPSISVOWLNNEEDHTGHTTRPOKDHTGDP 296

Db 277 PEVYVPPPPBEPBESDRTLCLQNFQGDGLLISNQHSHTTPLKNSNSQ 336

QY 297 SFFYSLMLJNKSTIEWKGNLVTCTVHNLPGSSTLEKSLHYSGN 342

Db 337 GFFIFSRLEVAKTWTQRKQFTCQVTHEALQKPRLEKTISTSGN 382

RESULT 5

Ig epsilon chain C region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Accession: S38864

R:Kipp, B.; Becker, W.; Schlaak, M.

R:Submitted to the EMBL Data Library, November 1993

A:Description: Combination of a defined specificity and desired isotype by cloning of a

A:Reference number: S38864

A:Accession: S38864

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-548 <KIP>

C:Cross-references: EMBL:Z27197; NID:9116537; PID:CA817881; PID:9340782

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:353-421/Domain: immunoglobulin homology <IMM>

QY 36.7%; Score 682; DB 2; Length 548;

Best Local Similarity 43.0%; Pred. No. 3.6e-43;

Matches 142; Conservative 52; Mismatches 122; Indels 14; Gaps 4;

QY 12 LPESGETVTPPTVCLFHSSCDPQCD--AHSTIQLLCLVSGFSPAKVHTWLQGQEAEN 69

Db 229 VPEVSSSVFIPPKPK-----DVLTRSTIQYCFIYGHILNDVSYWLMDREITD 278

QY 70 LFPYTRPRCEGGCQTRVTHEALPGSNTYCHVRNGSIFEDSRKCADSNPRG 129

RESULT 4

EHMS

Ig epsilon chain C region (version 1) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Accession: A02144

R:Liu, F.T.; Albrandt, K.; Sutcliffe, J.G.; Katz, D. H.

Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

Proc. Natl. Acad. Sci. U.S.A. 79, 7852-7856, 1982

Db	279	TIAQTVLKEE-GKLASTCSKUNITEQWMSESTFICKVTEQGDYLAHTFRRCPDPHEPRG	337	Db	365	KSNGSNQFFFFSRLVEYAKTLWTRQRQFTCQVTHEALIQKPRKLEKTTSTSIGN	417
Qy	130	VSAYLSPRSPFDLFIRKSPITLVLAPSCKTGNLTWSSASGKEVNHSTRKEERQNG	189	RESULT 7			
Db	338	VITYLIPSPPLDLYQANGAPKLTCLVVLDSEK-NVNTWNEQKETTSVASQWYTKHNTA	396	B46529			
Qy	190	TIYTSTLPGTDRDWEETCYOCTPHPLKPAPEYTMPLPPSPPEET	249	Ig Y heavy chain (7.8S) - duck			
Db	397	TTTSISIDEVAKDWIGEYGYQTIDPDPKPIVRSITKPGQRAPETVFPPEEES	456	N; Alternate names: Ig gamma chain (7.8S) C; Species: Anas platyrhynchos (domestic duck) C; Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 21-Jul-2000 C; Accession: B46529; R; Major, K.E.; Warr, G.W.; Higgins, D.A.			
Qy	250	GTTRTVTCILRGFYPSEISVONLFNNEEDHTGHHTTRPKDHEGTDPSPFLYSLMLVNGS	309	J. Immunol. 149, 2627-2633, 1992			
Db	457	EDRGLTLCIQLQNFFPEDSVQWNGDTLIRNSQHSTTPLKSNGSNRGGFIIFSRDEVAKI	516	A; Title: Structural relationship between the two IgY of the duck, Anas platyrhynchos: A; Reference number: A46529; PMID:9301786; MUID:315182			
Qy	310	IWEKGNLVTCRVTHEALPGSRTLEKSLHYS	339	A; Accession: B46529			
Db	517	IWTQRQQFCQVTHEALQPRKLEKTTIS	546	A; Status: preliminary A; Molecule type: mRNA A; Residues: 1-572 <MAG>			
RESULT 6				A; Cross-references: EMBL:X65219; NID:962442; PID:CAA46322; PID:962443			
EMHS				A; Experimental source: spleen			
C; Species: Mus musculus (house mouse)				C; Superfamily: immunoglobulin C region; immunoglobulin homology			
C; Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004				F:37-120/Domain: immunoglobulin homology <IMM>			
R; Ishida, N.; Ueda, S.; Hayashida, H.; Miyata, T.; Honjo, T.				Query Match 31.3%; Score 580.5; DB 2; Length 572;			
EMBO J. 1, 1117-1123, 1982				Best Local Similarity 38.2%; Pred. No. 1-4e-35;			
A; Title: The nucleotide sequence of the mouse immunoglobulin epsilon gene: comparison with the mouse immunoglobulin epsilon gene. #status predicted				Matches 124; Conservative 56; Mismatches 130; Gaps 9;			
A; Reference number: A90966; MUID:84236092; PMID:6329728				Qy 22 PPTVKLFFHSS-CDPRGDASHSTIQLCLVSYGSPDAKTVTFLVDQGELENLPYTTTRKRE 80			
A; Molecule type: DNA				Db 249 PPEYQVLLSSVVCSTLGD--DSVLLCITGFSPPPVVEWLVGAPA-HLYATMTRPQE 305			
A; Residues: 1-423 <ISH>				Qy 81 -GGOTFSLOSEYNTTQGOMMSNTTYCIVKH--NGSFEDSDSRKCADSNPRS--VSAYL 134			
A; Cross-references: UNIPROT:P06336				Db 306 AGSKTMYMATSQTNVWSREDWKAGKAFTCRVKHATGGTAQGHARFCPSGAQSCSPIQIFV 365			
A; Note: the sequence was determined from the germline gene				Qy 135 SRPEPDIFIRKSPITLVLAPSCTVNTIWSRASGKPVNTHSTKEEKFORNGTIVT 194			
C; Genetics:				Db 365 VPPSGSLTIRQDQAVLWNVN-PSDASLSLSTWTRKSGALRPDMVLTENGFTAS 424			
A; Introns: 91/1; 199/1; 307/1				Qy 195 STLPGVGTDWIEGETYQCRVTHPHLPRALMRSTTLPKGRLAPEVNLPPSPBETGTR- 253			
C; Complex: An immunoglobulin heterotetramer subunit consists of two identical light (κα) chains disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a superfamily: immunoglobulin C region; immunoglobulin homology				Db 425 SSLAISTQWMLAGERFTCTVQHDLPLFKGSIAKHGKVTAQPYIFFPRAEELAAEV 484			
C; Superfamily: duplication; Glycoprotein; heterotrimer; immunoglobulin				Qy 254 TVTLCLRGYPSETSVQMLFNEEDHTCHHTTRPKDQHDGTDPSFELYSRMVNUKSTWEK 313			
C; Keywords: duplication; Glycoprotein; heterotrimer; immunoglobulin				Db 485 TLTCVLRGQPVEREVQMLRNINSPVAEEFVTPPLCEPNQDGTFEFFLPSQTVPKSWQG 544			
F:16-77/Domain: immunoglobulin homology <IMM>				Qy 314 GNLYTRDVRVHEAL---SRRLEKS 355			
F:115-183/Domain: immunoglobulin homology <IMM>				Db 545 GVSYACMVYTHEGLPMRFTORPLQKT 569			
F:120-288/Domain: immunoglobulin homology <IMM>				RESULT 8			
F:125-336/Domain: immunoglobulin homology <IMM>				Qy 500 S00390 Ig gamma chain (clone 36) - chicken (fragment)			
F:133-84,167,239,262,417/Binding site: carbohydrate (Asn) (covalent) #status predicted				N; Alternate names: Ig nu chain Species: Gallus gallus (chicken)			
Qy 2 FHHHHHTLSPESGPVTTIPYTRPREGQFISLOSEVNITQGMMSNTTYCIVKHN 111				C; Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 11-Jan-2000			
Db 73 FTCHVTHPSFSENERTLVRPV---HSLSPWNSYIHRCDPNA-FHSTTQLYCIVGH 127				R; Parvari, R.; Aviri, A.; Lentner, F.; Ziv, E.; Tel-Or, S.; Burstein, Y.; Schecter, I.			
Qy 52 SPAKVHVTWLVDQEAENIIPYTRPREGQFISLOSEVNITQGMMSNTTYCIVKHN 111				EMBO J. 7, 739-744, 1988			
Db 128 ILNDVSVSMIMDREITDLAGVNLKEE-GKLASTCSKLNTEQWMSESTFCRTVSQ 186				A; Title: Chicken immunoglobulin gamma-heavy chains: limited VH gene repertoire, combination of genes			
Qy 112 GSIFEDSSRKCADSNSPRGVSYLSPSPFDLFIRKSPITLVLAPSCTVNTIWSRA 171				A; Reference number: S00390; PMID:88283642; MUID:315182			
Db 187 GDUYLAHTRCPHPEPRGAIYLIIPPSDLMQNGAKLTCLVWDESEK-NVNTWNEQ 245				A; Accession: S00390			
Qy 172 SGKEVNHSRKEKQNRGTLTVTSPYTRWIEGETYQCRVTHPHLPRALMRSTTLP 231				A; Molecule type: mRNA A; Residues: 1-504 <PAR>			
Db 246 KRTSVSASWYTKHNNATTSILPVAKDIEGYQCVQVDRPDPFPKIVSIT-LP 304				A; Cross-references: EMBL:X01714			
Qy 232 -GKRLLAPVWYMPSPSPETGTRTVCILRGYPSETSVQMLFNEEDHTCHHTTRPK 289				A; Note: this sequence was determined from the differentiated gene			
Db 305 QVSRSAPPVVFPPBEESEDERTRLCLIQFFPEDISSVWLGDKLINSQHSSTTPPL 364				C; Superfamily: immunoglobulin C region; immunoglobulin homology			
Qy 290 KDHGTDPSFLSPFLYSLVNLKSIWKGNLVTCRVTHEALPGSRTLEKLYHSGN 342				C; Keywords: immunoglobulin			

Query Match	28.9%	Score 535.5; DB 2; Length 504;	Db	151 WLRDGQVESEGVLTLPVVAETKGAGPATEISSMTITBDSWLSQSLYTCRVDRHGIFFD 210
Best Local Similarity	35.1%	Pred. No. 2.6e-32;	Db	117 DS--SRKCADSNPFGVSAYLSPRSPPFDLIRKSPPTITLVLVDLAPSKTGTVNLTWSRASG 173
Matches	118;	Conservative	Db	211 KNSVSSCETTPSGCIVPIAPFADPELSKARLICLVDT-TYCSLNLISWASHING 269
Ov	17 PVTIIPPTVRLFLH-SSCDPRGDAHSTIQQLCLVYSGFSFSAKHYTIVLWDQEAENLFPYTT 75	Qy	117 DS--SRKCADSNPFGVSAYLSPRSPPFDLIRKSPPTITLVLVDLAPSKTGTVNLTWSRASG 173	
Db	172 PVPPVAPPEQVQLHASSCTP--SQSESVELLCLVTFGFSASAEEVWLVDG--VGGLLYASQ 227	Db	211 KNSVSSCETTPSGCIVPIAPFADPELSKARLICLVDT-TYCSLNLISWASHING 269	
Ov	76 RPKREGQQFTSLOSEVNNTQGOMNSNTYCHYKH--NGSIFEDSSRKCADS---NPG 129	Qy	174 KPVNHSSTRKEBKQRNGTLTVTSLLEGPTRDIEGGTYQCRTVPHPLRALMRSTTKLPK 233	
Db	228 SPAVRSGSYTSLSSRNVNTSGDNEGRSKVSCVRPHPATNTVVEDHVKCPDGAQSCP-- 285	Db	270 KALDHMNNTIESHPATPSAMGEASVCAEWESEGEQFTCTVTHADLPLKHTISK--SR 327	
Ov	130 VSAYLSPRSPPFDLIRKSPPTITLVLVDLAPSKTGTVNLTWSRASGKPYTHSTEKEKORNG 189	Qy	234 RLAA--PEVYMLPPSPEE--TGTRTRTVTCLIRGFYPSSEISVQNLINNEDDHTGHHTTRP 288	
Db	286 IQLYAIPPSGELYTLSDALKRLCLVNN--PSDSLSSLVNTREXSGNLRDPMVLQEEFNG 344	Db	328 EVAKRPPAVTVLPFAAREQLVLRERSTVTCLVKGFSPADFVQWQCRGQPLSSDKVVTSA 387	
Ov	190 TLTVTSTLVGTRDWEGETYQCRVTHPHPLRALMRSTTKLCKRKLAPETVNLPPSPEET 249	Qy	289 QKDHGTDPSFLPSFLYSRMLVNSKSIWEGNLVTCRVYHEALP--GSRTLEKSLHYSAG 341	
Db	345 TYASSAVAVSTQOWLSEGRFTCVQHEDPLLSKSTYRNTGPTTLPFLIXPAPHEEL 404	Db	388 APEPQAPGLVFLTHSLTVTBEWDNSGETFCVYHEALPHMVTRVDSSTEGERV 443	
RESULT 10				
Qy	250 GTTR-TVTLIRGFYPSSEISVQNLINNEDDHTGHHTTRPQDH----GTDPSFLFY 301	Qy	19 mu chain C region - golden hamster	
Db	405 SLSRVYTLSCVLRGRPRDIEIRNIRDHRAYPAFEVTVLFEERTANGAGSDGDFEVY 464	C;Species: Mesocricetus auratus (golden hamster)		
Ov	302 SRMLVNSKTSWERGNLVTCTVYHEALP--GSRTLEK 334	C;Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Aug-1996		
Db	465 SKMSVETAKNGTGTACMAVHEALPMRFQSQTLOK 500	C;Accession: A02168		
RESULT 9				
MRBMB	IG mu chain C region, membrane-bound form - rabbit	A;Note: The sequence was determined from the germline gene for residues 105 and 324 as Val and Glu re		
C;Species: Oryctolagus cuniculus (domestic - rabbit)	C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1			
C;Date: 04-Dec-1986 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004	C;Superfamily: immunoglobulin C region; immunoglobulin homology			
R.Bernstein, K.E.; Alexander, C.B.; Reddy, E.P.; Mage, R.G.	C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin			
C;Accession: A02165; A02164	A;Title: Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of V-Ha2 a			
J.J. Immunol. 132, 490-495, 1984	A;Reference number: A02164; MUID:84098930; PMID:6418803			
A;Contents: a2 allele	A;Accession: A02165			
A;Molecule type: mRNA	A;Residues: 439-479 <BE2>			
A;Cross-references: UNIPROT : P04221	A;Accession: A02164			
A;Molecule type: mRNA	A;Residues: 1-438, 'GKPTLYNSLIMSDTASTCY' <BER>			
A;Note: the sequence of residues 1-438 was assumed to be identical with the corresponding C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1				
C;Superfamily: immunoglobulin C region; immunoglobulin homology	C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin			
F:21-92/Domain: immunoglobulin homology <IMM1>	F:130-202/Domain: immunoglobulin homology <IMM2>			
F:142-310/Domain: immunoglobulin homology <IMM3>	F:219/Domain: immunoglobulin homology <IMM4>			
F:449-459/Domain: carboxyl-terminal <CTS>	F:449-479/Domain: carboxyl-terminal bonds: interchain (to light chain) #status predicted			
F:28-50,137-200,249-308,356-418 Disulfide bonds: #status predicted	F:28-50,137-200,249-308,356-418 Disulfide bonds: #status predicted			
F:46,114,212-261,277,284/Binding site: carbohydrate (Asn) (covalent) #status predicted	F:46,114,212-261,277,284/Binding site: carbohydrate (Asn) (covalent) #status predicted			
F:296/Disulfide bonds: interchain (to heavy chain) #status predicted	F:296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted			
Query Match	26.8%; Score 497.5; DB 1; Length 479;	Db	117 NHSTKEEKQRNGTLTVTSLPVGTRDMEGETYQCRVTHPH-PLRALMRSTTKLPG-KRL 235	
Best Local Similarity	32.9%	Pred. No. 1.6e-29;	Db	269 ETKTYKLTESHPNGTFSAAEYANVCEWDSGKEFVTVTHDLPSQKKFISKPGRMKT 328
Matches	117; Conservative	Db	5 HHHHTLSPESGPV-TIIPPTVYKLFHSSCDPR---GDAHSTIQLI-CLVSGFSPAKVHVT 59	
Ov	94 HSNSNRDRLRVSPFDSEPPNVSVE--IIPRDGSFSSGTRSKRSRLCQATFSPQISVS 150	Qy	236 APEVYMLPPSPEE--TGTRTRTVTCLIRGFYPSSEISVQNLINNEDDHTGHHTTRPQKDHG 293	
Db	60 WLYDGQEAEN--LFPYTRKREGQFOTSFLOSEVNNTQGOMMSNTYCHVKGNSLIFE 116	Db	329 PPVYQPLAREQLTRELSEATVTLVKGFSPADFVQNLQRGQPLSDQKYVTSAPMREPQ 388	
Ov		Qy	294 TDPSFLYSRMLVNSKSIWEGNLVTCRVYHEALP--GSRTLEK 335	

369 APHYFTHSVLTVTEBWNNSGETYTCVGHALPHMVTERTVDRS 433

Db	RESULT 11 MERB Ig mu chain C region, secreted form - rabbit Species: Oryctolagus cuniculus (domestic rabbit) C:Date: 13-Aug-1986 #sequence_change 09-Jul-2004	A;Residues: 1-326 <ELL> A;Cross-references: UNIPROT:PO1859; GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; P A;Note: Lys-326 is probably removed posttranslationally R;Wang, A.-C.; Tung, E.; Fudenberg, H.H. J. Immunol. 125, 1048-1054, 1980
		A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f A;Reference number: A32809; MUID:81007873; PMID:6774012
		A;Contents: myeloma protein Till
		A;Molecule type: protein A;Residues: 1-19 'O' 21-57 'Z' 59 'A' 61-193 'D' 195-325 <WAN>
		A;Note: Trp-156 is at or near the complement-binding site R;Connell, G.E.; Parr, D.M.; Hofmann, T. Can. J. Biochem. 57, 758-767, 1979
		A;Title: The amino acid sequences of the three heavy chain constant region domains of a A;Reference number: A30752; MUID:80001357; PMID:113060
		A;Contents: myeloma protein Zinc
		A;Accession: A90752 A;Molecule type: Procollin A;Residues: 1-24 'E' 26-57 'EV' 60-85;132-171, 'ZZZZ',175, 'B',177-193, 'D',195-196, 'Q',198- A;Note: this sequence has since been revised R;Hofmann, T.; Parr, D.M. Mol. Immunol. 16, 923-925, 1979
		A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g A;Reference number: A33132; MUID:80114419; PMID:118920
		A;Contents: Zinc
		A;Accession: A90752 A;Molecule type: protein A;Residues: 238-245 R;Hofmann, T.; Parr, D.M. A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2. A;Reference number: A30253; MUID:72033500; PMID:490472
		A;Contents: annotation; myeloma protein Sa, disulfide bonds R;Frangione, B.; Milstein, C.; Pink, J.R.L. Nature 221, 145-148, 1969
		A;Title: Structural studies of immunoglobulin G. A;Reference number: A31157; MUID:69064124; PMID:5782707
		A;Contents: annotation; Sa, disulfide bonds C;Genetics: A;Gene: GDB:IGHG2 A;Cross-references: GDB:119338; OMIM:147110 A;Map position: 14q2.33-14q2.33
		C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a C;Superfamily: immunoglobulin C region, immunoglobulin homology <IM2> C;Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin F:121-92/Domain: immunoglobulin homology <IM1> F:2130-202/Domain: immunoglobulin homology <IM3> F:242-310/Domain: immunoglobulin homology <IM4> F:149-420/Domain: immunoglobulin homology <IM5> F:19-457/Disulfide bonds: interchain (to light chain) #status predicted F:28-90,137-200,249-30,356-418/Disulfide bonds: carbohydrate (Asn) (covalent) #status predicted F:349-420/Domain: immunoglobulin homology <IM4> F:296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted F:296/Disulfide bonds: interchain (to mu chain in another subunit) #status predicted
		Query Match Score 495.5; DB 1; Length 458; Best Local Similarity 33.1%; Pred. No. 2.2e-29; Matches 116; Conservative 61; Mismatches 148; Indels 25; Gaps 10;
Qy	5 HHHHTLSEPGV-TIIPPTKLFHSSCDP--GDAHTSIQICLVGFSPAKVHVT 59	
Db	94 HSNMRDVRVSPPFDSELPVNNTSVP--IPRDSFSSGTRSRQLCQATGFSQPKQISV 150	
Qy	60 WLVGDQEAEH--LFPTTTRPKREGOTFSLOSEVNITQOWMSSNTTYCHVKINGSIPE 116	
Db	151 WLVDQKVEVSGVLTKEVAGPATFISSMMLTIDESWLQSLYTLRVDHRGIFFD 210	
Qy	117 DS--SRKADSNSPRGVSYALSRSPPDFLRKSPPTICLVDFDASPKGTVNLTMSRASC 173	
Db	211 KVMSMSECTSPSPGIOVPIAPSADTFLSKSARLICLVDTL-TYGSININASHNG 269	
Qy	174 KPTNHSTREKERNGLTVTSTPLPVTRDWEGETYQRCHRTHPRALMRSTTKLPGK 233	
Db	270 KALDTHMNITESTHPNFAFSAMGEASVCAEDWESQGFTCTTHADLPPLKHTISK-SR 327	
Qy	234 RLA--PEVYMLPPSPEE--TGTRTRVCLRGFYPESEISYOWLNFNEEDHTGHHTTRP 288	
Db	328 EVAKHPAPVYLPARELIVLRESATVCLVGFSPADVTFQWQQRGQPSDSDRFTSAP 387	
Qy	289 QDKHGTDSFFLYSRLYNKSWEKGNLVTTCRVHEALP--GSRTLEKS 335	
Db	388 APEPQAPGIFTYHSTLTVTEEDWNNSGETFCVVGHEALPMVTERVDS 437	
	F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted	
	Query Match Score 26.2%; DB 1; Length 326; Best Local Similarity 36.2%; Prd. No. 6.7e-29; Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;	
Qy	35 RGDAHSTQQLCLYSGFGSPAKYHVTW---LVDGQEAENLFPYTTRKREGQQTLSQSE 90	
Db	16 RSIESESTAAAGLCLYKDFDEPEPYVSNNSGALTSG---VHTFFPAVL---QSSGLYLSVSS 68	
Qy	91 VNTQGQMSNSNTYTCYHVKH--NGSFEDSSRKCAASNPN-----RGVSAVLRSRSPF 140	
Db	69 VTVFSSNF GTQTYTCVNDHKPSNTKVDTKVERKCCYECPPCPAPPVAGPSVFLPPRPK 127	

RESULT 12
GBHU
IG Gamma-2 chain C region - human
C:Species: Homo sapiens (man)
C:Accession: A93906; A92809; A97052; A93132; A02148
R;Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain constant regions
A;Reference number: A93906; MUID:82157621; PMID:6804948
A;Molecule type: DNA

QY 141 D-LPIRKSPITCLVVDLAPSKGKTVNLWSRASGKPYVNHTSTRKEEKQRNGTLTVTSTLPV 199
 Db 128 DTNQNSRTPBEVTQVVDPSHEDPQFQWVYDVEVIRAKTIPREBQNSTRVSVTV 187
 QY 200 GTRDWIEGETYOCBVTHPHIPLRMRSTTKLPGKRLABEVKMLPPSSBE-TGTTTCTVCL 258
 Db 188 VHQDWLNGEYKCRVNSKGCLPAPLEKTSKTKCQQPREQVYLPPSSEEMTNQVSNTCL 247
 QY 259 IRGFYPSLISVQWLNNEDHTGHHTTRPQDHGTDSFLYSRMLVNSLWEKGNLVT 318
 Db 248 VKGYPSPDAVEVSNGOPEN-NYKTPPPMLD-SDQSFELYSKLTVDKSFWQQNFES 303
 QY 319 CRYVHEALPDSRTELEKSJHYSG 341
 Db 304 CSVNHEALHNHT-QKSLSLSPG 325

QY 141 D-LPIRKSPITCLVVDLAPSKGKTVNLWSRASGKPYVNHTSTRKEEKQRNGTLTVTSTLPV 199
 Db 128 DTNQNSRTPBEVTQVVDPSHEDPQFQWVYDVEVIRAKTIPREBQNSTRVSVTV 187
 A;Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
 A;Reference number: A90333; MUID:83157104; PMID:6299662
 A;Accession: A90933
 A;Molecule type: DNA
 A;Residues: 1-327 <ELL>
 A;Cross-references: UNIPROT:P01861
 A;Note: the sequence was determined from the germline gene
 R;Pink, J.R.L.; Butterly, S.H.; De Vries, G.M.; Milstein, C.
 Biochem. J. 117, 33-47, 1970
 A;Title: Human immunoglobulin subclases. Partial amino acid sequence of the constant
 A;Reference number: A90249; MUID:70207560; PMID:4192699
 A;Accession: A90249
 A;Molecule type: protein
 A;Residues: 1-30,-81-326 <PIN>
 C;Genetics:
 A;Gene: GIB:IGHG4
 A;Cross-references: GDB:119340; OMIM:147130
 A;Atom position: 1492-33-1492-33
 A;Introns: 99/1; 111/1; 221/1
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka
 chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: duplication; glycoprotein; immunoglobulin homology <IM1>
 P;20-85/Domain: immunoglobulin homology <IM1>
 P;99-110/Region: hinge
 F;134-203/Domain: immunoglobulin homology <IM2>
 F;240-307/Domain: immunoglobulin homology <IM3>
 F;14-/Disulfide bonds: interchain (to light chain) #status experimental
 F;27-83-141-201,247-305/Disulfide bonds: #status predicted
 F;105-109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F;177/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25 6% Score 476; DB 1; Length 327;
 Best Local Similarity 35.8%; Pred. No. 4.1e-28;
 Matches 116; Conservative 57; Mis matches 121; Indels 30; Gaps 10;

QY 35 RDGAHTSTIQLLCLIVSGFSPKAVWTV---LVDQEAENLFPTTRPKREGQTFSLQSE 90
 Db 16 RSTSTESTAAIGCLVRYDYFPEPVTVWSNNGALTSG---VTFPAVL---QSSGIVSLSSV 68

QY 91 VNITQWMSNSNTYTCVHRENS IFEDSRPKCADSNP-----RGVSAVLRSRSP 139
 Db 69 VTPVSSS-LGTTKTYCNVDHKPSNTKVDRVESKYGPPCPSCPAPEFLGGPSVFLFPPKP 127

QY 140 FD-LFIRKSPITCLVLDLAPSKGTVNLWSRASGKPYVNHTSTRKEEKQRNGTLTVTSTLP 198
 Db 128 KDTNMRSPTEVTCVTDQSQDEVQFTWVYDQCEVANAKTREFEEQNSTYRVVSLT 187

QY 199 VGTRDPIEGTYOCTVTHPHIPLRMRSTTKLPGKRLAPEVYMLPPSPE-TGTTTVC 257
 Db 188 VLHQDWLNGEYKCRVNSKGCLPSSTEKTSKAKQPREQVYTLPSQSEEMTNQVSCLC 247

QY 258 LARGFYPSETSVNLFNNEEDHTGHHTTRPOQHDTDSFFLYSMLVANKS1WEKGNLV 317
 Db 248 LVKGYPSPSDAVENWSNGOPEN-NYKTPPPVZD-SDGSSFLYSLRTVDSRWRQEGNVF 303

QY 318 TCRYTHEALGDSRTELEKSJHYSG 341
 Db 304 SCSYVHEALHNHT QKSLSLSPG 326

RESULT 15
 S14633
 Ig mu chain precursor, membrane-bound (clone 201) - human
 C;Species: Homo sapiens (man)
 C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 23-Jul-1999
 C;Accession: S11681; S0047
 R;Friedlander, R.M.; Nussenzweig, M.C.; Leder, P.
 Nucleic Acids Res. 18, 4278, 1990
 A;Title: Complete nucleotide sequence of the membrane form of the human IgM heavy chain
 A;Reference number: S14683; MUID:9033450; PMID:211596
 A;Accession: S14683

QY 141 D-LPIRKSPITCLVVDLAPSKGKTVNLWSRASGKPYVNHTSTRKEEKQRNGTLTVTSTLPV 199
 Db 128 DTNQNSRTPBEVTQVVDPSHEDPQFQWVYDVEVIRAKTIPREBQNSTRVSVTV 187
 QY 200 GTRDWIEGETYOCBVTHPHIPLRMRSTTKLPGKRLABEVKMLPPSSBE-TGTTTCTVCL 258
 Db 188 VHQDWLNGEYKCRVNSKGCLPAPLEKTSKTKCQQPREQVYLPPSSEEMTNQVSCLC 247
 QY 259 IRGFYPSLISVQWLNNEDHTGHHTTRPQDHGTDSFLYSRMLVNSLWEKGNLVT 318
 Db 248 VKGYPSPDAVEVSNGOPEN-NYKTPPPVZD-SDGSSFLYSLRTVDSRWRQEGNVF 303
 QY 319 CRYVHEALPDSRTELEKSJHYSG 341
 Db 304 SCSYVHEALHNHT QKSLSLSPG 326

RESULT 14
 G4H11
 Ig gamma-4 chain C region - human
 C;Species: Homo sapiens (man)
 C;Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 09-Jul-2004
 C;Accession: A90333; A90249; A02150
 R;Ellison, J.; Buxbaum, J.; Hood, L.

A;Molecule type: mRNA
 A;Residues: 1-627 <FR1>
 A;Cross-references: EML:X17115; NID:933450; PID:CAA34971.1; PID:g33451
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: immunoglobulin; membrane protein
 F;1-15/Domain: signal sequence #status predicted <SIG>
 F;16-627/Product: Ig mu chain #status predicted <IGM>
 F;34-117/Domain: immunoglobulin homology <IMM>

Query Match	25.6%	Score 475.5;	DB 2;	Length 627;
Best Local Similarity	31.4%;	Pred.	No. 9.9e-28;	
Matches	106;	Conservative	65;	Mismatches 142;
				Indels 25;
				Gaps 10;

```

Qy      17 PYTII---PPTVKLFHSSCDPR----GDAHSTIQLLCLVSGFSPLAKVHTWLVDQEAEN 69
Db      254 PLVIAELPPKYSVF---VPPADGFFENPRSKSLKICATQESPROIQSWLREBKQVG 310
Qy      70 LFPPYT---RPKREGQQTESLOSEYVNITQOMMSNTYTCVHGNSIP-EDSSRKCA 123
Db      311 --GVTTDQYQAEAKSGPTTYKVTSITLTIKESDWLQSMMFCRVDEHGLDFQQNASSMCV 368
Qy      124 DSNPRGVSAYLRSRPSPPDFIKSPPTITCIVDLSKGTYNLWRSASSGKPVNHSTRKE 183
Db      369 PDDDTAIRFAIPPSAFILTKSTKLTCLVTDLT-TYDSVTISWRQNGAVKTHNIS 427
Qy      184 EKORGTLTVTSTLPVGTRDIEGETYQCRYTHPHPLPRLMRSTKLPGKRL-APEVYML 242
Db      428 ESHPNATFSAVEASICEDDNNNSGERITCTVHTDLSPIKOTISRPKGVALHRDVYIL 487
Qy      243 PPSPEETG--TPTVTCLRGYPSELSVQWLFNEEDHITHHTTRQGDHGDPSFFL 300
Db      488 PPARQOLNIRESATITCLVGTGSPADYFVQNMORGQPLSPEKEYTSAPMSEPAQAGRYFA 547
Qy      301 YSRMLVNRKSIWEGNLNTCRVTHEALFG--SRTLEKS 335
Db      548 HSLLTVSEBEWNTEGETYTCVVAHEALPNRVTERTVDKS 585

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Search completed: November 14, 2004, 15:02:15
 Job time : 41 secs

Result No.	Score	Query	Match	Length	DB ID	Description
1	1038.5	56.0	428	1	EPC_HUMAN	P01854 homo sapien
2	1033.5	55.7	571	2	BAC85440	Bac85440 homo sapien
3	767.5	41.4	429	1	EPC_RAT	P01855 rat/rattus norvegicus
4	40.5	40.5	421	1	EPC_MOUSE	P06336 mus musculus
5	497.5	26.8	479	1	MICR_RABBIT	P04221 oryctolagus cuniculus
6	495.5	26.8	464	2	Q6M2F6	Cae45931 homo sapien
7	496.5	26.8	464	2	CABE5931	P03988 oryctolagus cuniculus
8	495.5	26.7	458	1	MUC_RABIT	Bac85395 homo sapien
9	493.5	26.5	454	2	BAC85395	Bac85443 homo sapien
10	493.5	26.6	468	2	BAC85483	Q6P6C4 homo sapien
11	483.5	26.3	465	2	Q6P6C4	Aah6235 homo sapien
12	488.5	26.3	465	2	AAHF2335	P01859 homo sapien
13	486.5	26.2	326	1	GC2_HUMAN	Q6N093 homo sapien
14	486.5	26.2	417	2	Q6N093	Cae45777 homo sapien
15	486.5	26.2	417	2	CABE5777	Cae45777 mesocricetus auratus
16	493	26.0	454	1	MUC_MESAU	P01861 homo sapien
17	482.5	26.0	337	2	Q95i34	P01871 homo sapien
18	482.5	26.0	472	2	BAC85393	Bac85393 equus caballus
19	479.5	25.8	473	2	Q8TC63	P018593 homo sapien
20	479.5	25.8	476	2	Q6MzX7	Q6mzX7 homo sapien
21	479.5	25.8	476	2	CABE5900	Cae45200 homo sapien
22	476	25.6	327	1	GC4_HUMAN	P01861 homo sapien
23	475.5	25.6	454	1	MUC_HUMAN	P01871 homo sapien
24	470	25.3	614	2	Q7TM76	Q7TM76 mus musculus
25	469	25.3	455	1	MUC_MOUSE	P01872 mus musculus
26	469	25.3	476	1	MUC_MOUSE	P01873 mus musculus
27	469	25.3	613	2	Q8vCX7	Q8vCX7 mus musculus
28	467	25.2	548	2	BAD00196	Bad00196 camelus dromedarius
29	465	25.1	375	2	Q8ETT1	Q8ETT1 homo sapien
30	465	25.1	480	2	Q6PF1	Q6PF1 homo sapien
31	465	25.1	480	2	AAH16381	Aah16381 homo sapien

Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665 (1982).
 [7]
 RN 3D STRUCTURE MODELING.
 RP MEDLINE=87089848; PubMed=3796618;
 RX Padlan E.A.; Davies D.R.;
 RA "A model of the Fc of immunoglobulin E.";
 RT Mol. Immunol. 23:1063-1075(1986).
 RL -!- SIMILARITY: Contains 4 immunoglobulin-like domains.
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 CC
 DR EMBL; L00022; AAB59424.1; ALT_INIT.
 DR PIR; A22271; BHNU.
 DR PDB; 1F6A; X-ray; B/D-207-428.
 DR PDB; 1FP5; X-ray; A=07-428.
 DR PDB; 1G84; NMR; A=106-210.
 DR PDB; 1IGB; Model; A/B-.-.
 DR PDB; 100V; X-ray; A/B=102-428.
 DR Genew; HGNC:5522; IGHE.
 DR MIM; 147180.
 DR GO; GO:00323; F:Antigen binding; NAS.
 DR GO; GO:0006555; P:Immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl1.
 DR InterPro; IPR003006; Ig_MHC.
 DR SMART; SM00007; Ig; 4.
 DR PROSITE; PS5835; Ig_LIKE; 4.
 DR PROSITE; PS00290; Ig_MHC; 3.
 KW 3D-structure; Direct protein sequencing; Glycoprotein;
 KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
 FT NON_TER 1 1 Ig-like 1.
 FT DOMAIN 6 103
 FT DOMAIN 112 210
 FT DOMAIN 214 218
 FT DOMAIN 324 423
 FT DISULFID 14 14 Ig-like 4.
 FT DISULFID 15 105 Interchain (with a heavy chain).
 FT DISULFID 29 85 Interchain (with a heavy chain).
 FT DISULFID 121 121
 FT DISULFID 135 193 Interchain (with a heavy chain).
 FT DISULFID 209 209 Interchain (with a light chain).
 FT DISULFID 239 299
 FT DISULFID 405 405 N-linked (GLCNAC. .).
 FT CARBOHYD 21 21 N-linked (GLCNAC. .).
 FT CARBOHYD 49 49 N-linked (GLCNAC. .).
 FT CARBOHYD 99 99 N-linked (GLCNAC. .).
 FT CARBOHYD 146 146 N-linked (GLCNAC. .).
 FT CARBOHYD 252 252 N-linked (GLCNAC. .).
 FT CARBOHYD 275 275 N-linked (GLCNAC. .).
 FT VARIANT 359 359 W -> L (possible polymorphism).
 FT /FTId=VAR_003885.

FT STRAND 113 119.
 FT STRAND 130 138
 FT STRAND 148 151
 FT TURN 152 153
 FT STRAND 154 156
 FT HELIX 158 160
 FT STRAND 163 165
 FT STRAND 173 181
 FT TURN 182 186
 FT TURN 187 188
 FT STRAND 191 196
 FT STRAND 201 206
 FT STRAND 218 221
 FT HELIX 226 230
 FT TURN 231 232

FT STRAND 236 244
 FT STRAND 252 257
 FT TURN 258 259
 FT STRAND 267 272
 FT TURN 274 275
 FT STRAND 278 285
 FT HELIX 288 292
 FT TURN 293 294
 FT STRAND 297 302
 FT TURN 304 305
 FT STRAND 310 314
 FT STRAND 322 322
 FT STRAND 325 330
 FT STRAND 334 334
 FT TURN 335 336
 FT STRAND 337 337
 FT STRAND 340 351
 FT STRAND 356 361
 FT TURN 362 363
 FT STRAND 364 365
 FT HELIX 368 370
 FT STRAND 371 373
 FT STRAND 377 378
 FT STRAND 384 393
 FT HELIX 394 399
 FT STRAND 403 408
 FT TURN 410 411
 FT TURN 413 415
 FT STRAND 417 422
 SQ 428 AA; 47019 MW; 25C4CA072AA558A0 CRC64;
 SQ

Query Match 56.0%; Score 1038.5; DB 1; Length 428;
 Best Local Similarity 62.4%; Pred. No. 9.3e-72;
 Matches 201; Conservative 41; Mismatches 73; Indels 7; Gaps 4;
 Matches 201; Conservative

Qy 22 PPTVKLFHSSCDPGRDHSTIQQLCLNSGFSPAKVHNTWLYDQEAENLFPYTRKREG 81
 Db 111 PPTVKLISSSCDQGHFPPTIQLCLSDGYGTINTWLQVND--VDLSTASTTOE 168
 Qy 82 GOFESLQSEBVNTITQGOVMSNTYTCHYRNGSIFEDSRKCADSNSPKVNSTRKEKORNGLTVTSTLPVGT 201
 Db 169 GELASTQSPLTSQKHNLSDRHTYCQTYQHTEEDSTKCADSNFRGVSAVLRSRSPFD 228
 Qy 142 LFIPKSPPTITCLVYDAPSKGTIVNLTWSRASGPVNSTRKEKORNGLTVTSTLPVGT 201
 Db 229 LFIPKSPPTITCLVYDAPSKGTIVNLTWSRASGPVNSTRKEKORNGLTVTSTLPVGT 288
 Qy 202 RDWIEGETYQCRVTHPHIPRALMRSSTKLPGKRLAPVYMLPPSPPEGT--TRTVCLI 259
 Db 289 RDWIEGETYQCRVTHPHIPRALMRSSTKLPGKRLAPVYAF-ATPWPSPGSRDKRTLACLI 347
 Qy 260 RGFPSPSEISQVLENNEEDHTGHHTTRPQDHGTDDSFPLYSRMLVNSMEKGNNVTC 319
 Db 348 QNFNPEDISQVNLNEQQLPDARHSTQPRKTGGS--GFFVFSRLEVTRAEMEQKDFIFIC 405
 Qy 320 RYVHEALPGSRTLEKSLLIYSAG 341
 Db 406 RAVHEAASPSQTQVARAVSVNPG 427

RESULT 2
 ID BAC5440 PRELIMINARY;
 ID BAC5440 PRELIMINARY;
 AC
 DT 02-MAR-2004 (TREMBLrel. 27, Created)
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DT 02-MAR-2004 (TREMBLrel. 27, Last annotation update)
 DE CDNA FLJ27315 fis, Clone TMS06851, highly similar to Ig epsilon chain
 DE C region.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primata; Catarrini; Homidae; Homoo.
 NCBI_TaxID=9606;
 NCBI_TaxID=9606;

[1] SEQUENCE FROM N.A.
P TISSUE=Thymus;
C Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
A Mizuno S., Moriyaga M., Kawamura M., Sugiyama T.,
A Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
A Sugano S.;
A Submitted (JUL-2003) to the ENBL/GenBank/DDBJ databases.
EMBL: AK130825; BAC5440.1; -
SEQUENCE 571 AA; 62602 MW; E920DD06277B8D2FF CRC64;

Query Match 55.7%; Score 1033.5; DB 2; Length 571;
Best Local Similarity 61.9%; Pred. No. 3.2e-71; Indels 13; Gaps 7;
Matches 205; Conservative 41; Mismatches 72; Indels 13; Gaps 7;

Y 15 SGPVIIIPPTVYLPHSSCDPQDAH--STIQLCLIVSGPSPAKAVHTWLYDGQEAEFLFPV 72
b 249 SGDFT--PPTVKILQSSCD--GGEHEPTTQILCLVSGYTGCTINTWLQEQVMD--VD 302
b 363 YLSRSPFDLFRKSPITCLVLDAPSKGIVNLTSRASGPVNISTREEKQRNGTLF 422
Y 73 YTTRPREGGQTFSLOSEVNITQGQWMSNTYTCVYKHNGSLFEDDSRKCADSNPRGVSA 132
b 303 LSTASTQEGELASTQESTLSQLQHMLSDRVTYCQVTVQHTPESDKKCADSNPRGVSA 362
Y 133 YLSRSPFDLFRKSPITCLVLDAPSKGIVNLTSRASGPVNISTREEKQRNGTLT 192
b 363 YLSRSPFDLFRKSPITCLVLDAPSKGIVNLTSRASGPVNISTREEKQRNGTLF 422
Y 193 VTSILVGTRWIEGETYQCRVTHPLPRAALMRSTTKLPGRKLAPVYMLPPSPEETGT- 251
b 423 VTSILVGTRWIEGETYQCVTHPLPRAALMRSTTKLPGRKLAPVYMLPPSPEETGT- 481
Y 252 -TRTYCLIRGFYPSLSVQNLFNNEEDHTGHHTTRPOQDHGTDPSFPLYSRMLVNSI 310
b 482 DKRTLAGLNQMPEDSVQNLHENQQLPDARHSTTQPRKTGS--GFFVFSRLVEYRAE 539
Y 311 WERGNLTTCRVTHAEGPSVNLKELEKSHYSG 341
b 540 WEQXDFICRAYHAAASPQTWQRAYVNPQ 570

RESULT 3
D EPC_RAT STANDARD; PRT; 429 AA.
P01855; 21-JUL-1986 (Rel. 01, Created)
C 21-JUL-1986 (Rel. 01, Last sequence update)
T 10-OCT-2003 (Rel. 42, Last annotation update)
T 19 epsilon chain C region.
IS Rattus norvegicus (Rat).
IS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
NCBI TaxID=10116;
L [1] SEQUENCE FROM N.A. (IMMUNOCYTOMA IR2).
L STRAIN=LOU/C/WSL; MEDLINE=83182019; PubMed=820340;
L LINE=83064537; PubMed=6292865;
L Hellman L., Pettersson U., Engstrom A., Karlsson T., Bennich H.;
L "Structure and evolution of the heavy chain from rat immunoglobulin
T Nucleic Acids Res. 10:6041-6049(1982).
N N SEQUENCE OF 168-342 FROM N.A. (MYELOMA IR162).
N MEDLINE=83182019; PubMed=820340;
N Kindsvogel W.R., Reddy E.P., Moore J.M., Faust C.H. Jr.;
N "A cloned cDNA probe for rat immunoglobulin epsilon chain:
T construction, identification, and DNA sequence.";
T DNA 1:335-343(1982).
T [2] SEQUENCE OF 205-306 FROM N.A. (MYELOMA IR162).
T MEDLINE=82174576; PubMed=68032318;
T Hellman L., Pettersson U., Bennich H.;
T "Characterization and molecular cloning of the mRNA for the heavy
T chain of rat immunoglobulin E.";
T Proc. Natl. Acad. Sci. U.S.A. 79:1494-1498(1982).
C - SIMILARITY: Contains 4 immunoglobulin-like domains.

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RT (epsilon) chain of rat immunoglobulin E.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1494-1498(1982).
CC DR EMBL: J00744; AAA41379.1; ALT_INIT.
DR PIR; A93442; EART.
DR ASSP; P01854; 2-FPS.
DR InterPro; IPR0110; Ig-like.
DR InterPro; IPR03597; Ig_C1.
DR InterPro; IPR03006; Ig_MHC.
DR Pfam; PF00047; Ig_4.
DR SMART; SM00407; IgC1_1.
DR PROSITE; PS50835; Ig_LIKE_4.
DR PROSITE; PS00299; Ig_MHC_3.
KW Immunoglobulin C region; Immunoglobulin domain; Repeat.
FT NON_TER 1 1
FT DOMAIN 1 1
FT DOMAIN 6 89
FT DOMAIN 103 201
FT DOMAIN 205 305
FT DOMAIN 314 414
FT DOMAIN 168 168
FT CONFFLICT 308 308
FT CONFFLICT 429 AA; 48671 MW; D2970B34EF8A72B0 CRC64;
SQ Query Match 41.4%; Score 767.5; DB 1; Length 429;
Best Local Similarity 45.8%; Pred. No. 7.3e-55; Gaps 4;
Matches 151; Conservative 54; Mismatches 114; Indels 11; Gaps 1;
QY 17 PTIILPTVKLHSSCDPQDAHSTTQIOLCLVSGFSPAKVHTWLYDGQEAEFLFPVTR 76
Db 97 PVNITKETVDLHSSCDPNA-FHSTIQLCYCFYGHQNDVS1HWLMIDRKI----YETH 150
QY 77 PK---PEGGOFSLQEBVNITQGQWMSNTYTCVYKHNGSLFEDDSRKCADSNPRGVSA 132
Db 151 AQNLVLEEGKLASTI8RINTTQQNMSESTPKTYSQGENYWAHRRCSDDEPRGVIT 210
QY 133 YLSRSPFDLFRKSPITCLVLDAPSKGIVNLTSRASGPVNISTREEKQRNGTLT 192
Db 211 YLIPSPFDLQDENGTPKLTCLVLDL-ESEENITVTVWRERKSIGASQRSTGHNNATTS 269
QY 193 VTSTLPGTRDIEGETYQCRVTHPLPRAALMRSTTKLPGRKLAPVYMLPPSPEETGT 252
Db 270 ITSLIPDADKTDIEGGQCRVTHPLPRAALMRSTTKLPGRKLAPVYMLPPSPEETGT 252
QY 253 RYVTCILRGTFYPSLSEISVQWLNEEDHTGHHTTRPOQDHGTDPSFPLYSRMLVNSIWE 312
Db 330 RTUTCLQNFEDISVQWLQSKLPIKPSQSTTTPKYKNGNQRFPPFSRUEVKAINT 389
QY 313 KGNLVTCRVVHALPGERTLEKSLHSGAN 342
Db 390 QTKQFCTCERVIBALREPRKLERTISKSLGN 419

RESULT 4
ID EPC_MOUSE STANDARD; PRT; 421 AA.
AC P01856; 21-JUL-1996 (Rel. 01, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Ig epsilon chain C region.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Muridae; Murinae; Mus.
OC NCBI TaxID=10090;

[1]	SEQUENCE FROM N.A.	RX MEDLINE=84226092; PubMed=6329728;	Db 191 AHTRRCPDHEPRGVITYLIPSPSLDLYQNGAPKLTCVYDSEK-NWVNTNQEKTSV 249
RA	Ishida N., Ueda S., Hayashida H., Miyata T., Honjo T.;	RA 177 NHSTREKEKQRNGTTLTVSTLPVGTRDWLEGETYQCRVTHPHLPRALMRSTTKLPGERLA 236	
RT	"The nucleotide sequence of the mouse immunoglobulin epsilon gene";	RT 250 SASQWYTKHANNATTSILSILPVVAKDMEGYQYCVTDHPDFPKVRSITKTPGORSQ 309	
RT	comparison with the human gene	EMBO J. 1:1117-1123 (1982).	
RN [2]	REVIEWS.		
RA	Honjo T.	RN 237 PEVYMLPPSPPEETGTTVTCIQRGFYSEISYOWLNEEDHTGHFTTRQKDHDTP 296	
RP	Submitted (APR-1986) to the EMBL/GenBank/DDJB databases.	Db 310 PEVVFPPBEEESDKRTRLTLCLQNFFEDDISYQWLGGKLNSQSTTPLKSNSNQ 369	
[3]	SEQUENCE OF 34-421 FROM N.A.	Db 297 SFEFLYSRMLVNUKSTWEKGNLVTCRUVHALPGSRTRLSKLYHSAGN 342	
RX	MEDLINE=83117774; PubMed=6818553;	Db 370 GFFIFSRLEVAKTLWTRQKQFTCQVIEHALQKPRKLERTISTLGN 415	
RA	Liu F.-T., Albrant K., Surcliffe J.G., Katz D.H.;		
RT	"Cloning and nucleotide sequence of mouse immunoglobulin epsilon chain cDNA.";		
RT	Proc. Natl. Acad. Sci. U.S.A. 79:7852-7856(1982).		
CC	EMBL; X01857; CAA5977_1; -.	OX [1]_TaxID=9386;	
DR	EMBL; X01857; CAA5978_1; -.	OX	
DR	PIR; A01144; EHMS5.	RN	
DR	PIR; A01145; EHMS5.	RX	
DR	PIR; A01146; EHMS5.	MEDLINE=84088330; PubMed=6118803;	
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CC	PROSITE; PS00835; Ig_LIKE; 4.	DT 01-MAR-1987 (Rel. 20, Last sequence update)	
DR	PROSITE; PS00290; Ig_MHC; 3.	DT 01-NOV-1991 (Rel. 20, Last annotation update)	
KW	Glycoprotein; Immunoglobulin C region; Immunoglobulin domain.	DB 19 mu chain C region encoded by and for membrane mu sequences.	
FT	NON_TER 1 1	DE Oryctolagus cuniculus (Rabbit).	
FT	DOMAIN . 1 90	OS Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lagomorpha; Leporidae; Oryctolagus.	
FT	DOMAIN 91 197	NCBI_TaxonID=9386;	
FT	DOMAIN 198 304	[1]	
FT	DOMAIN 305 421	RN	
FT	DISULFID 23 75	RX	
FT	DISULFID 121 180	RA Bernstein K.E., Alexander C.B., Reddy E.P., Mage R.G.;	
FT	DISULFID 226 285	RA "Complete sequence of a cloned cDNA encoding rabbit secreted mu-chain of VH2 allotype: comparison with VH1 and membrane mu sequences.";	
FT	DISULFID 330 392	RT J. Immunol. 132:480-495(1984).	
FT	CARBOHYD 43 43	RT -; ALTERNATIVE_PRODUCTS;	
FT	CARBOHYD 72 72	CC Event=Alternative splicing; Named isoforms=2;	
FT	CARBOHYD 84 84	CC Comment=During differentiation, B lymphocytes switch from expression of isoform Membrane-bound to isoform Secreted;	
FT	CARBOHYD 95 95	CC Name-Membrane-bound; Sequence=Displayed;	
FT	CARBOHYD 166 166	CC IsoID=P04221_1; Sequence=External;	
FT	CARBOHYD 238 238	CC Name-Secreted;	
FT	CARBOHYD 261 261	CC IsoID=P03988_1; Sequence=@isb-sib.ch.	
FT	CARBOHYD 365 365	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
FT	CARBOHYD 415 415	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
SEQUENCE	421 AA, 47320 MW,	CC EMBL; K01357; AAA31293..1;	
SQ	SEQUENCE 421 AA, 47320 MW,	CC PIR; A02165; MRBMB.	
Query Match	Best Local Similarity 40.5%; Score 751; DB 1; Length 421;	CC HSSP; P01861; 1AQD.	
Matches 155; Conservative 53; Mismatches 130; Indels 8; Gaps 4;	CC InterPro; IPR003359; Ig_c1.		
KW	Immunoglobulin domain; Transmembrane.	CC InterPro; IPR003006; Ig_MHC.	
FT	NON_TER 1 1	CC SMART; SM00407; Ig_c1; 2.	
FT		CC PROSITE; PS00835; Ig_LIKE; 4.	
FT		CC DR DISULFID 14 14 Interchain (with light chain) (Probable).	
FT		CC DR DISULFID 28 90 By similarity.	
FT		CC DR DISULFID 137 200 By similarity.	
QY	2 FHHHHHHHTSLPES-----GPVTHIPRYKLEHSSCDPREGDAHSTIOLCLVSGFSPAKV 56	QY 57 AVWVNDGGEAHLFPITPRKREGQTLOSSENITQGIMSSNTTYCHWANGSIFV 116	
Db	73 FICHHVTHPSNSRTLVRPWNITEPLLELLHSSCDPNA-FHSTIQLYCTYGHILNDY 131	Db 132 SVWLMDDREITOTLAQVYLKEE-GKLASTCSKLNTTEQWMSEESTFTKVTSQGVDYL 190	
Qy		Qy 117 DSSRKCADSNPREGVSAYLSRSPSPDLFIRSKPTITLVIDLAPSKGTVNLTWRSASKPV 176	

FT	DISULFID	219	219	Interchain (with heavy chain) (Probable).	DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
FT	DISULFID	249	308	By similarity	KW	Hypothetical protein.
FT	DISULFID	296	296	Interchain (with heavy chain) (Probable).	SEQUENCE	51099 MW; 2FCA72C668A0ABC CRC64.
FT	DISULFID	356	418	By similarity	SQ	
FT	CARBONYD	46	46	N-linked (Gln/Asn. . .) (Potential).	Query Match	26.8%; Score 496.5; DB 2; Length 464;
FT	CARBONYD	114	114	N-linked (Gln/Asn. . .) (Potential).	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
FT	CARBONYD	212	212	N-linked (Gln/Asn. . .) (Potential).	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
FT	CARBONYD	261	261	N-linked (Gln/Asn. . .) (Potential).	Qy	35 RGDAHSTIQQLCLVSGSPAKVHYTW---LVDGGEAENLFPYTRPKREGGQTFLQSE 90
FT	CARBONYD	277	277	N-linked (Gln/Asn. . .) (Potential).	Db	154 RSTSESTVALCLVQDFFPEPVTVWNSGALTSG---VHTFPAVL---QSSGLYSLSSV 206
FT	CARBONYD	284	284	N-linked (Gln/Asn. . .) (Potential).	Db	154 RSTSESTVALCLVQDFFPEPVTVWNSGALTSG---VHTFPAVL---QSSGLYSLSSV 206
FT	CARBONYD	57	57	Sequence 479 AA; 52351 MW; 689C637PA47B19PC CRC64;	Query Match	26.8%; Score 497.5; DB 1; Length 479;
FT	CARBONYD	57	57	Best Local Similarity 32.9%; Pred. No. 5.4e-30; Matches 117; Conservative 61; N mismatches 153; Indels 25; Gaps 10;	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
FT	CARBONYD	57	57	Query 94 HSNSTRDLVSPFDSELPPNVSF--IPPRDFSGGSSTRKRLICATGSPKQIISVS 150	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
FT	CARBONYD	60	60	WLVDGQAEN--LFPYTRPKREGGOTFSLOSEVNTITOGOMNNSNTYTCCHYKHNGSFE 116	Qy	91 VNIQGQWMSNTYTCVHKH---NGSIFEDSSRKADSNP---RGVSAYLRSRSPF 140
FT	CARBONYD	151	151	WLRDGQKVEGVLLPKPVEETKGGPATSISSMNTIDESWQSLSITCRDHRGIFED 210	Db	207 VTVTSSNF-GTQTYTCNVDDHKPSNTKVDKTVVERKCCVECPCPAPVAGPSVLFPPKP 265
FT	CARBONYD	117	117	DS---SRKCDSDNPRGVASYLRSRSPFDLFIKSPTICLVLAPSKGTNLTVWSASG 173	Query Match	26.8%; Score 498.5; DB 1; Length 480;
FT	CARBONYD	211	211	KVNSNSSECSTTPSGIVQFPIASSFADFLSKSARLICLVLT-TVGSNLTISWASHN 269	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
FT	CARBONYD	174	174	KPVNEHSTRKEEKQRNGTLTVSTLPVGTRDWBETTYQRTVTHPHALMESTTKLPGK 233	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
FT	CARBONYD	270	270	KALDTMMITESHPNATFSAMGEASVCAEDWESEQTCTVTHADLPPLKTISK--SR 327	Qy	91 VNIQGQWMSNTYTCVHKH---NGSIFEDSSRKADSNP---RGVSAYLRSRSPF 140
FT	CARBONYD	234	234	RLA---PEYMLPPSPEE-TGTRTRTVCLIRGPFSEISVQWLLENBEDHTGHHTTRP 288	Db	207 VTVTSSNF-GTQTYTCNVDDHKPSNTKVDKTVVERKCCVECPCPAPVAGPSVLFPPKP 265
FT	CARBONYD	328	328	EVAKHPAPPVLPVLPAREQVLRERATVILVKGPSPADPVQVQGRGQPLSSDKYTSAF 387	Query Match	26.8%; Score 499.5; DB 1; Length 488;
FT	CARBONYD	289	289	QKDHGTDPSRFYLSRMLVNSKWIKEGNLYTCRVHEALP--GSRTLEKSLHYSG 341	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
FT	CARBONYD	388	388	APEPOGAPGLYFTHSTLTVTEEDWNSGETFTCVGHEALPHMVTERTVKSTEGEVG 443	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
RESULT	6				Qy	35 RGDAHSTIQQLCLVSGSPAKVHYTW---LVDGGEAENLFPYTRPKREGGQTFLQSE 90
DR	Q6MZU6			PRELIMINARY; PRT; 464 AA.	Db	154 RSTSESTVALCLVQDFFPEPVTVWNSGALTSG---VHTFPAVL---QSSGLYSLSSV 206
AC	Q6MZU6			PRELIMINARY; PRT; 464 AA.	Query Match	26.8%; Score 496.5; DB 2; Length 464;
DT	05-TUL-2004			(TREMBLrel. 27, Created)	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
DT	05-TUL-2004			(TREMBLrel. 27, Last sequence update)	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
DE				Hypothetical protein DKFzp686C15213.	Qy	91 VNIQGQWMSNTYTCVHKH---NGSIFEDSSRKADSNP---RGVSAYLRSRSPF 140
GN				Name: DKFzp686C15213.	Db	207 VTVTSSNF-GTQTYTCNVDDHKPSNTKVDKTVVERKCCVECPCPAPVAGPSVLFPPKP 265
HN				Homo sapiens (Human).	Query Match	26.8%; Score 499.5; DB 1; Length 488;
OC				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Osteichthyes; Actinopterygii; Teleostei; Mammalia; Primata; Catarrhini; Hominidae; Homo.	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
NCBI TAXID	9606			Homosapiens; Human.	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
RN	[1]			SEQUENCE FROM N.A.	Qy	35 RGDAHSTIQQLCLVSGSPAKVHYTW---LVDGGEAENLFPYTRPKREGGQTFLQSE 90
RC				THE GERMAN HUMAN CDNA CONSORTIUM.	Db	154 RSTSESTVALCLVQDFFPEPVTVWNSGALTSG---VHTFPAVL---QSSGLYSLSSV 206
RG				Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.	Query Match	26.8%; Score 496.5; DB 2; Length 464;
RA				InterPro: IPR003597; IG-1.	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
RA				InterPro: IPR003006; IG-MHC.	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
RA				InterPro: IPR003596; IG-v.	Qy	91 VNIQGQWMSNTYTCVHKH---NGSIFEDSSRKADSNP---RGVSAYLRSRSPF 140
RA				Pfam: PF07654; Cl-set; 3.	Db	207 VTVTSSNF-GTQTYTCNVDDHKPSNTKVDKTVVERKCCVECPCPAPVAGPSVLFPPKP 265
RA				Pfam: PF00047; IG-4.	Query Match	26.8%; Score 498.5; DB 1; Length 488;
RA				SMART: SMD00409; IG-2.	Best Local Similarity	36.5%; Pred. No. 6.2e-30;
RA				SMART: SMD00407; IG-1.	Matches	118; Conservative 58; Mismatches 118; Indels 29; Gaps 11;
RA				PROSITE; PS50535; IG_LIKE; 4.	Qy	91 VNIQGQWMSNTYTCVHKH---NGSIFEDSSRKADSNP---RGVSAYLRSRSPF 140

Db	177 VSNNSGALTSG--VHTFPAVL--QSSGLYSLSSVVTPSSNF-GTQTYTCNDHKPS	228	RESULT 11
Qy	111 NGISFEDSSRKCADSNP-----RGVAYLSRSPSPFD-LFIRKSPTICLYVIDLAPSKGK 162	Q6P6C4	PRELIMINARY;
Db	229 NTRDKTVERKCCYECPPAPVAGPSVLFFPKPKDTLMISRTEPVTCVYDVSHEPD P 288	ID	Q6P6C4;
Qy	163 TVNLTWSRASGKPKYNHSTKEKEKQRNGTLTVTSTLPVGRDWEGETYQCRYTHPHLPRA 222	AC	Q6P6C4;
Db	289 EVQENWVYGVVEHAKTKPREEFNSTRVSVLTVYHODWLNGKEYCKVSNKGKLPAP 348	DT	05-JUL-2004 (TREMBLrel. 27; Last sequence update)
Qy	223 LMRSTTKLGKRLAPEYMLPPSPEE-TGTTTPTCLIRGFYSEISIVQLWNNEEDHTG 281	DT	05-JUL-2004 (TREMBLrel. 27; Last annotation update)
Db	349 IEKTISKTKQGPREFQVYTLPPSREEMTNKNOVSLTCLYKGFPSDIAVEWSNGOPEN- 406	DE	Hypothetical protein.
Qy	282 HHTTTRPQKDHDGIDPSEFFYSLMLVNKTSIWERKNLVTRVHEALPGSRTEKSLHYSG 341	OS	Homo sapiens (Human).
Db	407 NYKTPPMID-SDGSFFYSLKLTVDXSRWQONVFSSVHEALNHYT-QKSLSLSPG 463	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID:9606;
Qy	BAE85483 PRELIMINARY; /	OX	NCBI_TaxID:9606;
Db	BAE85483; 02-MAR-2004 (TREMBLrel. 27; Last sequence update)	RN	SEQUENCE FROM N.A.
Qy	BAE85483; 02-MAR-2004 (TREMBLrel. 27; Last annotation update)	RP	RP
Db	CDNA FL29011 fis. clone DMC03382, highly similar to Ig gamma-2 chain C region.	TISSUE=Spleen;	TISSUE=Spleen;
Qy	Homo sapiens (Human).	RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
Db	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID:9606;	RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
Qy	SEQUENCE FROM N.A.	RN	[2]
Db	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.
Qy	SEQUENCE FROM N.A.	RC	SEQUENCE FROM N.A.
Db	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.	RL	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
Qy	EMBL AX131045; BAC85483.1; CB3A94413B6C36CA CRC64;	DR	Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
Db	SEQUENCE 468 AA; 51715 MW;	DR	EMBL BC061335; AAH02335.1; -.
Qy	Score 493.5 ; DB 2 ; Length 468 ;	DR	InterPro; IPR003599; Ig.
Db	Best Local Similarity 34.7% ; Prd. No. 1..le-29 ;	DR	InterPro; IPR007110; Ig-like.
Qy	Matches 124; Conservative 66; Mismatches 134; Indels 33; Gaps 13;	DR	InterPro; IPR013597; Ig-C1.
Db	5 HHHTTLSLDESG-PVTIPIPTVK--LPHSSCDPFGDAHSTIQLLCHVGFSPAKYHVTW 60	DR	InterPro; IPR003006; Ig_MHC.
Qy	124 YYYGLDWTGQGPVTIATASTKGPSVFLAPDCSRSTISETAALGLIVKDVFPEPTVSW 183	DR	InterPro; IPR003596; Ig_V.
Db	61 -----LVDQEAENILFPYTRPREGCGTFLOSEVNITQGOMMSNTYTCVYKH--NGS 113	DR	Pfam; PF007654; Cl-sets; 3.
Qy	184 NSALALTSG--VHTFPAVL--QSSGLYSLSSVVTPSSNF-GTQTYTCNDHKPSNTK 235	DR	Pfam; PF00047; Ig; 4.
Db	SEQUENCE 468 AA; 51325 MW;	DR	SMART; SM00409; Ig; 2.
Qy	114 IFDSSRKCADSNP-----RGVAYLSRSPSPFD-LFIRKSPTICLYVIDLAPSKGTVN 165	DR	SMART; SM00407; IgCl; 3.
Db	236 VDKTVERKCCVCEPPCPAPVAGPSVLFFPKPKDTLMISRTEPVTCVYDVSHEPD P 295	DR	SMART; SM00406; IgV; 1.
Qy	166 LTWSRASKPKVNHSSTRKEKEKQRNGTLTVTSTLPVGRDWEGETYQCRYTHPHLPALMR 225	DR	PROSITE; PS50835; Ig_LIKE; 4.
Db	296 FNYVGDGEVHAKTKPREEFNSTRVSVLTVYHODWLNGKEYCKVSNKGKLPAPIEK 355	DR	PROSITE; PS00390; Ig_MH; UNKNOWN_2.
Qy	226 STTKLPGKRLAPEYMLPPSPEE-TGTTTPTCLIRGFYSEISIVQLWNNEEDHTGHFT 284	KW	Hypothetical protein.
Db	356 TISKTKGOPREPVVYTPSPREEMTNKQVSLTCLVGFYPSDIAVESSNQOPEN- NYK 413	SEQUENCE 465 AA;	FDDB9348ADC37E6D CRC64;
Qy	7 HHTTLSLDESG-PVTIPIPTVK--LPHSSCDPFGDAHSTIQLLCHVGFSPAKYHVTW 60	Query Match	26.3%; Score 488.5 ; DB 2 ; Length 465;
Db	131 HGTL -----VTVSSASTKGPSVFLAPDCSRSTISETAALGLIVKDVFPEPTVSWNSG 183	Best Local Similarity 35.0% ; Pred. No. 2..6e-29 ;	Best Local Similarity 35.0% ; Pred. No. 2..6e-29 ;
Qy	61 LIVDQEAENILFPYTRPREGCGTFLOSEVNITQGOMMSNTYTCVYKH--NGS 113	Matches 124; Conservative 61; Mismatches 130; Indels 39; Gaps 13;	Matches 124; Conservative 61; Mismatches 130; Indels 39; Gaps 13;
Db	184 ALTSG--VHTFPAVL--QSSGLYSLSSVVTPSSNF-GTQTYTCNDHKPSNTKVDK 235	7 HHTTLSLDESG-PVTIPIPTVK--LPHSSCDPFGDAHSTIQLLCHVGFSPAKYHVTW 60	7 HHTTLSLDESG-PVTIPIPTVK--LPHSSCDPFGDAHSTIQLLCHVGFSPAKYHVTW 60
Qy	117 DSSRKADSNP-----RGVAYLSRSPSPFD-LFIRKSPTICLYVIDLAPSKGTVN 165	Db 131 HGTL -----VTVSSASTKGPSVFLAPDCSRSTISETAALGLIVKDVFPEPTVSWNSG 183	Db 131 HGTL -----VTVSSASTKGPSVFLAPDCSRSTISETAALGLIVKDVFPEPTVSWNSG 183
Db	285 TTRPKDGHGTDPSFFYSLRMLYKNSKTMKEKGNLVTRVHEALPGSRTEKSLHYSG 341	Qy 61 LIVDQEAENILFPYTRPREGCGTFLOSEVNITQGOMMSNTYTCVYKH--NGS 113	Qy 61 LIVDQEAENILFPYTRPREGCGTFLOSEVNITQGOMMSNTYTCVYKH--NGS 113
Qy	414 TPPMLD-SDGSFFYSLKLTVDXSRWQONVFSSVHEALNHYT-QKSLSLSPG 467	Db 184 ALTSG--VHTFPAVL--QSSGLYSLSSVVTPSSNF-GTQTYTCNDHKPSNTKVDK 235	Db 226 STTKLPGKRLAPEYMLPPSPEE-TGTTTPTCLIRGFYSEISIVQLWNNEEDHTGHFT 284

QY D-LFIRKSPTITCLVVDLAPSRTKGVNLTVNLSRASGKPVNHTSTRKEEKORGTLTVTSTLTV 199
 Db 219 DTLMISRTEVTCTVVDDPSHEDPEVQNNWYVGVEVNAKTPRESEFNSTFRVSVLT 278
 QY 200 GTRDIEGETTYQCRVTHPHLPRALMRSTTKLPGRKLAPEVYMLPPSPEE-TGTTRTVTCL 258
 Db 279 VHQDWLNGKEYKCKVSNGKLPAPIEKTISRTKGQPREQQVTLPPSRSEEMTKNOVSLTCL 338
 QY 259 IRGFYPSETSVQWLLENNEEDHTGHHTTRPQDHGTDPSFLYSLYMLVNSIWEKGNLVT 318
 Db 339 VKGFPSPSDAVENTNGOEN-NYKUTPPMILD--SDGSFFLYSKLTVDSRWOQGNVFS 394
 QY 319 CRVYHEALGSRTLEKSLHYSG 341
 Db 395 CSVNHEALHNHT-QKSLSLSPG 416

RESULT 15

CAE5777

PRELIMINARY;

ID CAE5777; PRIT; 417 AA.

AC CAE5777;

DT 02-MAR-2004 (TREMBirel 27, Created)

DT 02-MAR-2004 (TREMBirel 27, Last sequence update)

DT 02-MAR-2004 (TREMBirel 27, Last annotation update)

DE Hypothetical protein DKFZP86I04196 (Fragment).

GN DKFZP86I04196.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

NCBII TaxID=9606; NCBI TaxID=9606;

OX -;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Human esophagus tumor;

RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,

RA Fobo G., Han M., Wiemann S., Submitted (Aug-2003) to the EMBL/GenBank/DDBJ databases.

RL EMBL; BXc40623; CAE45777.1; -.

KW Hypothetical protein.

FT NON TER 1

SQ 417 AA; 46061 MW; C4518EE44CFBB83C CRC64;

SEQUENCE

26.2%; Score 486.5; DB 2; Length 417;

Best Local Similarity 36.2%; Pred. 3.2e-29;

Matches 117; Conservative 57; Mismatches 120; Indels 29; Gaps 11;

QY 35 RGDAHTIQQLCLVSGFSIAKRVHTW---LVDGQEAENLFPTTRPKREGQTSLOSE 90

Db 107 RSTSESTAALGCLVKDYDFEPVTVWSNGALTSG--VHTPAVL---QSSGLYSLSSV 159

Qy 91 VNITGQWMSNTYCHVGH---NGSIFEDSSRKCADSNP-----RGVASYLSRPSPF 140

Db 160 VTVPSSNF-GTQTYTCNVDKPSMTKVDTVERKCCVECPGPAPPAGPSVLFPPKP 218

Qy 141 D-LFIRKSPTITCLVVDLAPSRTKGVNLTVNLSRASGKPVNHTSTRKEEKORGTLTVTSTLTV 199

Db 219 DTLMISRTEVTCTVVDDPSHEDPEVQFWYVDGVEVNAKTREREQNSTFRVSVLT 278

Qy 200 GTRDIEGETTYQCRVTHPHLPRALMRSTTKLPGRKLAPEVYMLPPSPEE-TGTTRTVTCL 258

Db 279 VHQDWLNGKEYKCKVSNGKLPAPIEKTISRTKGQPREQQVTLPPSRSEEMTKNOVSLTCL 338

Qy 259 IRGFYPSETSVQWLLENNEEDHTGHHTTRPQDHGTDPSFLYSLYMLVNSIWEKGNLVT 318

Db 339 VKGFPSPSDAVENTNGOEN-NYKUTPPMILD--SDGSFFLYSKLTVDSRWOQGNVFS 394

Qy 319 CRVYHEALGSRTLEKSLHYSG 341

Db 395 CSVNHEALHNHT-QKSLSLSPG 416

Abp96591	Brushtail	ABP96591	6
Aao19668	GE2 fusio	Aao19668	6
Abp96584	Duckbillie	ABP96584	6
Aao19667	Human IgE	Aao19667	6
Aau80286	Human IgE	Aau80286	6
Aau80285	Human IgE	Aau80285	5
Aau80284	Human IgE	Aau80284	5
Par83559	FC (epsi-5)	Par83559	5
Aar75225	Human IgE	Aar75225	2
Aar77241	Human IgE	Aar77241	2
Aab03642	Human IgE	Aab03642	2
Bind25768	Binding d	Bind25768	1
Aap80291	Interleuk	Aap80291	1
Aao19666	Human IgE	Aao19666	1
Asm78863	Human Ig-	Asm78863	1
Aau80283	Human IgE	Aau80283	1
Aam50940	Human imm	Aam50940	1
Aae35113	Human imm	Aae35113	1
Add84440	ADD84440	Add84440	1
Adp48440	ADD48440	Adp48440	1
Adp97382	Human IgE	Adp97382	1
Adp97382	Human IgE	Adp97382	1
GenCore version 5.1.6			
Copyright (c) 1993 - 2004 Compugen Ltd.			
protein - protein search, using sw model			
on:	November 14, 2004, 14:55:18 ; Search time 157 Seconds		
	(without alignments)		
	781.436 Million cell updates/sec		
title:	US-09-401-636-8		
reflect score:	1856		
quence:	1 EFPHHHHHTLSPESGPVTI.HEALPGSRTLEKSLHYSAGN 342		
oring table:	BLOSUM62		
Gapext 0.5	Gapext 0.5		
arched:	2002273 seqs, 358729299 residues		

maximum DB seq length: 9
maximum DB seq length: 200000000

st-processing: Minimum Match 0% Maximum Match 100%

1 - genesept1880s *

* 26 *

Genes 2001; 4: 169-175

6: geneseqp2003as:*

8: Genesep2004s:
2-
8: Genesep2004s:
2-

- 1 -

Searched		Query		Match		Length		DB		ID		Description	
Searched	No.	Score	%	Match	Length	DB	ID	DB	ID	DB	ID	Description	
Aab06205				AAB06205	3	AAB06205		Aab06205		Immungen-h			
Adf90035				ADF90025	8	ADF90025		Adf90035		OPOSSUM-h			
Adn00646				ADN00646	8	ADN00646		Adn00646		OPOSSUM-h			
Adf90033				ADF90033	8	ADF90033		Adf90033		OPOSSUM-h			
Adn00654				ADN00654	8	ADN00654		Adn00654		OPOSSUM-h			
Ahf90031				AHF90031	8	AHF90031		Ahf90031		OPOSSUM-h			
Adf90035				ADF90035	8	ADF90035		Adf90035		OPOSSUM-h			
Adn00656				ADN00656	8	ADN00656		Adn00656		OPOSSUM-h			
Adn00652				ADN00652	8	ADN00652		Adn00652		OPOSSUM-h			
Adf90039				ADF90029	8	ADF90029		Adf90039		OPOSSUM-h			
Ahf90037				AHF90037	8	AHF90037		Ahf90037		OPOSSUM-h			
Ahn0658				ADH0658	8	ADH0658		Ahn0658		OPOSSUM-H-P			
Adm00650				ADM00650	8	ADM00650		Adm00650		OPOSSUM-O			
Adn00661				ADN00661	8	ADN00661		Adn00661		H-OOC-H-D			
Aab6228				AAB6228	3	AAB6228		Aab6228		Immungen-h			
Aab06207				AAB06207	3	AAB06207		Aab06207		Immungen-h			
Aab03644				AAB03644	3	AAB03644		Aab03644		OPOSSUM-I			
Aab06206				AAB06206	3	AAB06206		Aab06206		Immungen-h			
Abp96587				ABP96587	6	ABP96587		Abp96587		OPOSSUM-I			
Adf90022				ADF90022	8	ADF90022		Adf90022		OPOSSUM-I			
Adn00643				ADN00643	8	ADN00643		Adn00643		OPOSSUM-I			
Adf90027				ADF90027	8	ADF90027		Adf90027		OPOSSUM-I			
Adn00648				ADN00648	8	ADN00648		Adn00648		OPOSSUM-I			
Aab06202				AAB06202	3	AAB06202		Aab06202		Immungen-h			
Aab06201				AAB06201	2	AAB06201		Aab06201		Immungen-h			
Aab06200				AAB06200	2	AAB06200		Aab06200		Immungen-h			

ALIGNMENTS

LT 1
6205 AAB06205 standard; protein; 342 AA.
AAB06205;
12-SEP-2003 (revised)
22-NOV-2000 (first entry)
Immunogenic peptide consisting of opossum CH2, human CH3 and opossum CH4.
Human: opossum: immunoglobulin E: IgE; vaccination; infection; allergy;
Human: opossum: immunoglobulin G: IgG; vaccination; infection; allergy;

Didelphis virginiana.
Homo sapiens.
Chimeric.

WO20005722-A2.

11-MAY-2000.
99WO-SB001896.

21-OCT-1999;
99US-010652P.

02-NOV-1998;
99US-01401636.

22-SEP-1999;
(RESI-) RESISTENTIA PHARM AB.

Hallman LT;

WPI; 2000-365342/31.

Immunogenic polypeptides useful for preventing the harmful effects of immunogenic polypeptides. Biotechnology

The present sequence is an immunogenic peptide consisting of the heavy chain constant regions 2 and 4 of the opossum IgE and the heavy chain constant region 3 from the human. It was shown to cause a stronger polyclonal anti-self IgE response than peptides consisting of the same regions from one mammal. Immunogenic peptides, particularly those consisting of different heavy chain constant regions, can be used for vaccination in humans, against bacterial and viral infections and allergies, such as asthma, fur, pollen and food allergies and eczema. (Updated on 12-SSP-2003 to standardise OS field)

SQ	Sequence 342 AA;	CC host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric polypeptides are provided.
Query Match	Score 1856; DB 3; Length 342;	When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.
Best Local Similarity	100.0%; Pred. No. 5.4e-146;	
Matches 342; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 EPHHHHHHTLSPLPSSGPVIIIPPTVKLHSSCDPRGDAHSTIQLICNSGSSPAKTVHNT 60	XX SQ Sequence 338 AA;
Db	1 EPHHHHHHTLSPLPSSGPVIIIPPTVKLHSSCDPRGDAHSTIQLCLVSGRSPAKTVHNT 60	Query Match 96.2%; Score 1786; DB 8; Length 338;
Qy	61 LVDGGEAENLFPYTRPKEGGQFPLSLOSEVN.TQGMWMSNTYTCVRAKNGSIFEDSSR 120	Best Local Similarity 99.4%; Pred. No. 3.6e-140;
Db	61 LVDGGEAENLFPYTRPKEGGQFPLSLOSEVN.TQGMWMSNTYTCVRAKNGSIFEDSSR 120	Mismatches 0; Indels 2; Gaps 1;
Qy	121 KCADSNPVGYSAYLSPRSPLDFLRKSPITCLVVDLAPSKGTVNLTVWASGKPVNTHST 180	Matches 334; Conservative 0;
Db	121 KCADSNPVGYSAYLSPRSPLDFLRKSPITCLVVDLAPSKGTVNLTVWASGKPVNTHST 180	Indels 0; Gaps 1;
Qy	181 RKEEKQRNSTLTVTSTLPGTDRDIEGYTQCRVTHPHLPRALMRSTKLPGKRLAPEVY 240	XX Qy 9 TLSLPESGPVIIIPPTVKLPHSSCDPREDAHSTIQLCLVSGSSPAKTVHNTVDPGQAE 68
Db	181 RKEEKQRNGNGLTVTSTLPGTDRDIEGYTQCRVTHPHLPRALMRSTKLPGKRLAPEVY 240	Db 3 TLSLPESGPVIIIPPTVKLPHSSCDPREDAHSTIQLCLVSGSSPAKTVHNTVDPGQAE 62
Qy	241 MLPPSPEETGTTRTVTCILRGFPESEISQWLJNNEEDHTGHHTTTRPKDQHGTDPSFFL 300	Db 69 NLFPYTRPKREGOTFSLOSEVNITQGMWMSNTYTCVRAKNGSIFEDSSRKCADSNPR 128
Db	241 MLPPSPEETGTTRTVTCILRGFPESEISQWLJNNEEDHTGHHTTTRPKDQHGTDPSFFL 300	Db 63 NLFPYTRPKREGOTFSLOSEVNITQGMWMSNTYTCVRAKNGSIFEDSSRKCADSNPR 122
Qy	301 YSRMLVNKSTIWEKGNLVTVRVCVHEALPSSRTLEKSLHYSGN 342	Db 129 GVSAYLSPRSPLDFLRKSPITCLVVDLAPSKGTVNLTVWASGKPVNTHSTKEEORN 188
Db	301 YSRMLVNKSTIWEKGNLVTVRVCVHEALPSSRTLEKSLHYSGN 342	Db 123 GVSAYLSPRSPLDFLRKSPITCLVVDLAPSKGTVNLTVWASGKPVNTHSTKEEORN 182
RESULT 2		Db 189 GTLTIVTSTLPVGTDWIEGETYQCRVTHPHLPRALMRSTKLPGKRLAPEVYMLPSP 246
ADF90025		Db 183 GTLTIVTSTLPVGTDWIEGETYQCRVTHPHLPRALMRSTKLPGKRLAPEVYMLPSP 242
ID ADF90025	standard; protein; 338 AA.	Qy 247 EETGTTRTVTCILRGFPESEISQWLJNNEEDHTGHHTTTRPKDQHGTDPSFLYSLRMV 306
AC ADF90025;		Db 243 EETGTTRTVTCILRGFPESEISQWLJNNEEDHTGHHTTTRPKDQHGTDPSFLYSLRMV 302
XX		Qy 307 NKSIMBKGNLVTCVHEALPGSRTLEKSLHYSGN 342
XX		Db 303 NKSIMBKGNLVTCVHEALPGSRTLEKSLHYSGN 338
DT 26-FEB-2004	(First entry)	RESULT 3 ADNO0646
DE Opossum-human chimeric IgE polypeptide.		ID ADNO0646 standard; protein; 338 AA.
XX		XX
KW IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic; antiallergic; dermatological.		AC ADNO0646;
XX		XX
OS Chimeric.		DT 17-JUN-2004 (first entry)
OS Didelphis virginiana.		XX
OS Homo sapiens.		DE OSO Protein, SEQ ID 6.
XX		XX
PN WO2003039966-A2.		KW Antiallergic; Vaccine; self-IgE; ORO; OSO; allergy.
XX		XX
PD 27-NOV-2003.		OS Synthetic.
XX		XX
PP 15-MAY-2003; 2003WO-IB002503.		PN WO2004022094-A1.
XX		XX
PR 21-MAY-2002; 2002US-0382552P.		DE 05-SEP-2002; 2002US-0408648P.
XX		XX
PA (RESI-) RESISTENTIA PHARM AB.		PA (RESI-) RESISTENTIA PHARM AB.
XX		XX
DR 2004-04-24196/04.		PT Hellman LT, Persson S, Gansson A;
DR N-PDB; ADF90024, ADF90023.		XX
XX		PT WPI; 2004-248376/23.
PT cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.		DR N-PSDB; ADN00645.
PT New host cell comprising a nucleic acid vector comprising a		XX
PT New composition comprising a self-IgE polypeptide and an aluminum		PT compound, useful for inducing an anti self-IgE antibody response in a
PT mammal for treating or preventing allergies.		XX
XX		XX
PS Claim 3; SEQ ID NO 6; 23pp; English.		PS Claim 3; Fig 8; 102pp; English.
XX		XX
CC The present sequence is the protein sequence of an opossum CH2-human CH3-		XX
CC opossum CH4 (OSO) chimeric IgE polypeptide. A vector comprising DNA		XX
CC encoding OSO can be used for recombinant production this chimeric IgE in		XX

XX	Heilmann LT;	Persson S,	Gansson A;		PN WO2003095966-A2.
XX	WPI; 2004-248376/23.			XX	PD 27-NCV-2003.
DR	N-PSDB;	ADN00653.		XX	PF 15-MAY-2003; 2003WO-IB002503.
XX	PT New composition comprising a self-IgE polypeptide and an aluminum			XX	PR 21-MAY-2002; 2002US-0382552P.
PT compound, useful for inducing an anti self-IgE antibody response in a				XX	(RESI-) RESISTENTIA PHARM AB.
PT mammal for treating or preventing allergies.				XX	PA
XX	PI Lundgren M, Fuentes A,	Magnusson A;		XX	PI Lundgren M, Fuentes A,
PS	Claim 3; Fig 16; 102pp; English.			XX	WPI; 2004-042496/04.
XX	The present invention relates to a composition comprising a polypeptide			XX	New host cell comprising a nucleic acid vector comprising a
CC	and an aluminum compound, where the polypeptide comprises a self-IgE			XX	CH2-human CH3-human CH3-polypetide (modOSO).
CC	polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide)			CC	The coding sequence for modOSO contains point mutations in the human
CC	ADN00643 ADN00645 ADN00650 ADN00652 ADN00654 ADN00656 ADN00658 or			CC	CH3 domains that abolish mast cell receptor binding. A vector comprising
CC	ADN00661). Administration of the composition to a mammal reduces the			CC	DNA encoding modOSO can be used for the recombinant production of the
CC	level of detectable free IgE in the mammal. The composition is useful for			CC	chimeric IgE in host, e.g. CHO, cells. The invention provides methods and
CC	inducing an anti self-IgE antibody response in a mammal for treating or			CC	molecules related to expressing chimeric IgE proteins. Nucleic acid
CC	preventing allergies. The present sequence is an OSO protein, used to			CC	vectors, host cells, and methods for producing chimeric IgE polypeptides
CC	illustrate the invention. The OSO-H protein contains an opossum CH4 IgE			CC	are provided. When administered to a mammal, the chimeric polypeptides
CC	domain followed by a human CH3 IgE domain contained by an opossum CH4 domain.			CC	can reduce the IgE antibody effects of IgE-related diseases such as
XX	The OSO-H protein also contains a C-terminal polyhistidine tag.			CC	asthma, allergies and eczema.
Sequence 347 AA;				XX	Sequence 557 AA;
Qy	99 NLFPYTRPKREGGQTFSLOSEVNITQGMMSNTYTCVKHNGSIFEDSRKCADSNPR	128	Query Match 95.5%; Score 1772; DB 8;	Qy	95.5%; Score 1772; DB 8;
Db	63 NLFPYTRPKREGGQTFSLOSEVNITQGMMSNTYTCVKHNGSIFEDSRKCADSNPR	122	Best Local Similarity 98.5%; Pred. No. 9_9e-139;	Db	Length 557;
Db	63 NLFPYTRPKREGGQTFSLOSEVNITQGMMSNTYTCVKHNGSIFEDSRKCADSNPR	122	Matches 328; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	Db	
Qy	122 GVSAYLRSRSPFDLFIKRSPITCLLVLWDAPSKGTVNLWRSASGPVHNSTRKEEKQRN	188	Qy	10 LSPLPSEGPTTIPPKVLFHSSCDPGRDAHSTIOLCLVSGFSPAKVHTWLVGDQAEIN	69
Db	123 GVSAYLRSRSPFDLFIKRSPITCLLVLWDAPSKGTVNLWRSASGPVHNSTRKEEKQRN	182	Db	225 IDIPSPGPTTIPPKVLFHSSCDPGRDAHSTIOLCLVSGFSPAKVHTWLVGDQAEIN	284
Qy	189 GTLTIVTSTLPGVTDWIEGBTYQCRVTHFLPRAIMSTKL--PGKRLAPEVYMLPPSP	246	Qy	70 LPFTTRPYBREGGQTFSLOSEVNITQGMMSNTYTCVKHNGSIFEDSRKCADSNPR	129
Db	183 GTLTIVTSTLPGVTDWIEGBTYQCRVTHFLPRAIMSTKL--PGKRLAPEVYMLPPSP	242	Db	285 LPFTTRPYBREGGQTFSLOSEVNITQGMMSNTYTCVKHNGSIFEDSRKCADSNPR	344
Qy	247 BETGTRTRTCLLIRGFPPEBISVWHLPGSRTLEKSLHYAGN 342	306	Qy	130 VSAYLRSRSPFDLFIKRSPITCLLVLWDAPSKGTVNLWRSASGPVHNSTRKEEKQRN	189
Db	243 BETGTRTRTCLLIRGFPPEBISVWHLPGSRTLEKSLHYAGN 338	302	Db	345 VSAYLRSRSPFDLFIKRSPITCLLVLWDAPSKGTVNLWRSASGPVHNSTRKEEKQRN	404
Qy	307 NKS1WEKGNIWTCVWHEALPGSRTLEKSLHYAGN 342	309	Qy	190 TLTVTSPLPVGTRWIEGBTYQCRVTHFLPRAIMSTKL--PGKRLAPEVYMLPPSPET	249
Db	303 NKS1WEKGNIWTCVWHEALPGSRTLEKSLHYAGN 338	309	Db	405 TLTVTSPLPVGTRWIEGBTYQCRVTHFLPRAIMSTKL--PGKRLAPEVYMLPPSPET	464
RESULT 6			Qy	250 GTTRTVCCLIRGFYFSEISYQWLNNNEEDHTGHHTTRFQKDGTIDPSPSET	309
ADF90031	ID ADF90031 standard; protein; 557 AA.		Db	465 GTTRTVCCLIRGFYFSEISYQWLNNNEEDHTGHHTTRFQKDGTIDPSPSET	342
XX	XX		Db	525 IWEKGNLVTCRVEALPGSRTLEKSLHYAGN 557	524
AC	AC		Qy	310 IWEKGNLVTCRVEALPGSRTLEKSLHYAGN 342	
DT	26-FEB-2004 (first entry)		Db		
DE	Opossum-human chimeric IgE polypeptide.				
XX	IgE; immunoglobulin; antibody; opossum; human; vaccine; antigenic; antiallergic; mutant; mutein.				
XX	Chimeric.				
XX	Synthetic.				
XX	Didelphid; virginiana.				
XX	Homo sapiens.				

IGE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic; antiasthmatic; dermatological.

Chimeric.
Didephis virginiana.
Homo sapiens.

WO2003096966-A2.

27-NOV-2003.

15-MAY-2003; 2003WO-IB002503.

21-MAY-2002; 2002US-0382552P.

(RESI-) RESISTENTIA PHARM AB.

Lundgren M, Fuentes A, Magnusson A;

WPI: 2004-042496/04.
 N-PSDB; ADF90034.

New host cell comprising a nucleic acid vector comprising a cytomegalovirus promoter, an Ig leader sequence, an insert sequence or SV40 late polyadenylation sequence, useful in producing a chimeric Ig polypeptide.

Claim 3; SEQ ID NO 16; 23pp; English.

The present sequence is the protein sequence of an opossum CH2-human CH3-opossum CH2-human CH3-opossum CH4 (OOSO) chimeric IgE polypeptide. A vector comprising DNA encoding OOSO can be used for recombinant production of the chimeric IgE in host, e.g. CHO, cells. The invention provides methods and materials related to expressing chimeric IgE proteins. Nucleic acid vectors, host cells, and methods for producing chimeric IgE polypeptides are provided. When administered to a mammal, the chimeric polypeptides can reduce the IgE antibody effects of IgE-related diseases such as asthma, allergies and eczema.

Sequence 557 AA;	Query Match	95.5%	Score 1772;	DB 8;	Length 557;
	Best Local Similarity	98.5%	Pred. No. 9	9e-139;	
Matches 328	Conservative	?	Mimic	?	Trd17
Score 1772	DB 8	Length 557	No.	None	0

Db	525 IWEKGNLVCRVHEALPSRTLEKSLLHYSGN	557	Db	405 TLTVTSTLPVGTRDWEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVMLPPSPEET	464
RESULT 9 ADN00652 ID ADN00652 standard; Protein; 557 AA.	XX	QY 250 GTTRTTCILRGFYPSEISYQWLNFNEEDHTGHHTTREQDKDHGTDPSFFLYSRMLYNKS 309	QY 250 GTTRTTCILRGFYPSEISYQWLNFNEEDHTGHHTTREQDKDHGTDPSFFLYSRMLYNKS 309		
AC ADN00652;	XX	Db 465 GTTRTTCILRGFYPSEISYQWLNFNEEPHTGHHTTREQDKDHGTDPSFFLYSRMLYNKS 524	Db 465 GTTRTTCILRGFYPSEISYQWLNFNEEPHTGHHTTREQDKDHGTDPSFFLYSRMLYNKS 524		
DT 17-JUN-2004 (first entry)	XX	QY 310 IWEKGNLVCRVHEALPSRTLEKSLLHYSGN 342	QY 310 IWEKGNLVCRVHEALPSRTLEKSLLHYSGN 342		
DE modOSO protein, SEQ ID 12.	XX	Db 525 IWEKGNLVCRVHEALPSRTLEKSLLHYSGN 557	Db 525 IWEKGNLVCRVHEALPSRTLEKSLLHYSGN 557		
XX Antiallergic; Vaccine; self-IGE; ORO; OSO; allergy.	XX	RESULT 10 ADF90029	RESULT 10 ADF90029		
XX Synthetic.	XX	ID ADF90029 standard; protein; 566 AA.	ID ADF90029 standard; protein; 566 AA.		
XX PN WO2004022094-A1.	XX	XX XX	XX XX		
XX PD 18-MAR-2004.	XX	AC ADF90029;	AC ADF90029;		
XX PF 02-JUN-2003; 2003WO-IB003075.	XX	XX DT 26-FEB-2004 (first entry)	XX DT 26-FEB-2004 (first entry)		
XX PR 05-SEP-2002; 2002US-0408648P.	XX	XX DE Opossum-human chimeric IgE polypeptide.	XX DE Opossum-human chimeric IgE polypeptide.		
XX PA (RESI-) RESISTENTIA PHARM AB.	XX	XX KW IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;	XX KW IgE; immunoglobulin; antibody; opossum; human; vaccine; antiallergic;		
XX PI Hellman LT, Persson S, Gansson A;	XX	XX KW antiasthmatic; dermatological; mutant; mutein.	XX KW antiasthmatic; dermatological; mutant; mutein.		
XX DR WPI: 248376/23.	XX	XX XX	XX XX		
DR N-PDB; ADN00551.	XX	OS Synthetic.	OS Synthetic.		
PT New composition comprising a self-IGE polypeptide and an aluminum compound, useful for inducing an anti self-IGE antibody response in a mammal for treating or preventing allergies.	PT	OS Dideethyls virginiana.	OS Dideethyls virginiana.		
PT PI Lundgren M, Fuentes A, Magnusson A;	PT	OS Homo sapiens.	OS Homo sapiens.		
PT PR 21-MAY-2002; 2002US-0382552P.	PT	XX XX	XX XX		
PT PA (RESI-) RESISTENTIA PHARM AB.	PT	XX XX	XX XX		
PS DR 27-NOV-2003.	PS	PD 27-NOV-2003.	PD 27-NOV-2003.		
XX XX	XX	XX XX	XX XX		
CC PT 15-MAY-2003; 2003WO-IB002503.	CC	DR WPI: 2004-042496/04.	DR WPI: 2004-042496/04.		
CC PT 21-MAY-2002; 2002US-0382552P.	CC	XX XX	XX XX		
CC PA (RESI-) RESISTENTIA PHARM AB.	CC	PT PR 21-MAY-2002; 2002US-0382552P.	PT PR 21-MAY-2002; 2002US-0382552P.		
XX XX	XX	XX XX	XX XX		
CC PS Lundgren M, Fuentes A, Magnusson A;	CC	XX XX	XX XX		
CC PT 27-NOV-2003.	CC	CC CC	CC CC		
CC DR WPI: 2004-042496/04.	CC	CC CC	CC CC		
CC PT PR 21-MAY-2002; 2002US-0382552P.	CC	CC CC	CC CC		
CC PA (RESI-) RESISTENTIA PHARM AB.	CC	CC CC	CC CC		
XX XX	XX	CC CC	CC CC		
CC The present invention relates to a composition comprising a polypeptide and an aluminium compound, where the polypeptide comprises a self-IGE polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide: ADN00643, ADN00646, ADN00650, ADN00654, ADN00656, ADN00658 or ADN00661). Administration of the composition to a mammal reduces the level of detectable free IgE in the mammal. The composition is useful for inducing anti self-IGE antibody response in a mammal for treating or preventing allergies. The present sequence is an OSO protein, used to illustrate the invention. The modOSO protein contains an opossum CH2 IgE domain followed by a human CH3 IgE domain followed by an opossum CH2 IgE domain followed by a human CH3 IgE domain that abolish mast cell receptor binding. The modOSO protein also contains point mutations in the human CH3 domains that abolish mast cell receptor binding.	CC	CC The present sequence is the protein sequence of an opossum CH2-human CH3 opossum CH2-human CH4 chimeric IgE polypeptide including a C-terminal polyhistidine sequence (modOSO-H). The coding sequence for modOSO-H contains point mutations in the human CH3 domain that abolish mast cell receptor binding. A vector comprising DNA encoding modOSO-H SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.	CC		
CC Sequence 557 AA;	CC	CC PT 27-NOV-2003.	CC PT 27-NOV-2003.		
XX XX	XX	CC XX	CC XX		
CC The present sequence is the protein sequence of an opossum CH2-human CH3 opossum CH2-human CH4 chimeric IgE polypeptide including a C-terminal polyhistidine sequence (modOSO-H). The coding sequence for modOSO-H contains point mutations in the human CH3 domain that abolish mast cell receptor binding. A vector comprising DNA encoding modOSO-H SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.	CC	CC The present sequence is the protein sequence of an opossum CH2-human CH3 opossum CH2-human CH4 chimeric IgE polypeptide including a C-terminal polyhistidine sequence (modOSO-H). The coding sequence for modOSO-H contains point mutations in the human CH3 domain that abolish mast cell receptor binding. A vector comprising DNA encoding modOSO-H SV40 late polyadenylation sequence, useful in producing a chimeric IgE polypeptide.	CC		
CC Sequence 557 AA;	CC	CC XX	CC XX		
XX XX	XX	CC XX	CC XX		
CC Query Match 95 5%; Score 1772; DB 8; Length 557;	CC	CC XX	CC XX		
CC Best Local Similarity 98 5%; Pred. No. 9_9e-138; Mismatches 2; Conservative 3; Indels 0; Gaps 0;	CC	CC XX	CC XX		
CC Matches 328; Conservative 2; Indels 0; Gaps 0;	CC	CC XX	CC XX		
QY 10 LSLPSEGPTTIPPTVKLFHSSCDPRGDASHSTIQQLCLVSGFSPAKVFVTWLVDGQAEN 69	QY 10 LSLPSEGPTTIPPTVKLFHSSCDPRGDASHSTIQQLCLVSGFSPAKVFVTWLVDGQAEN 69				
Db 225 IDIPESGPVTIPPTVKLFHSSCDPRGDASHSTIQQLCLVSGFSPAKVFVTWLVDGQAEN 284	Db 225 IDIPESGPVTIPPTVKLFHSSCDPRGDASHSTIQQLCLVSGFSPAKVFVTWLVDGQAEN 284				
QY 70 LFPTTRPKREGGQTLSQSVNNTQGOMNSNNYTCVTHNGSIIFEDSRKCADSNPRG 129	QY 70 LFPTTRPKREGGQTLSQSVNNTQGOMNSNNYTCVTHNGSIIFEDSRKCADSNPRG 129				
Db 285 LFPTTRPKREGGQTLSQSVNNTQGOMNSNNYTCVTHNGSIIFEDSRKCADSNPRG 344	Db 285 LFPTTRPKREGGQTLSQSVNNTQGOMNSNNYTCVTHNGSIIFEDSRKCADSNPRG 344				
QY 130 VSAYLRSRSPEDLFIRKSPPTCLVNDAPSKGTYNLTWMSRASCKPVNHSRKERQNG 189	QY 130 VSAYLRSRSPEDLFIRKSPPTCLVNDAPSKGTYNLTWMSRASCKPVNHSRKERQNG 189				
Db 345 VSAYLRSRSPEDLFIRKSPPTCLVNDAPSKGTYNLTWMSRASCKPVNHSRKERQNG 404	Db 345 VSAYLRSRSPEDLFIRKSPPTCLVNDAPSKGTYNLTWMSRASCKPVNHSRKERQNG 404				
QY 190 TLTVTSTLPVGTRDWEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVMLPPSPEET 249	QY 190 TLTVTSTLPVGTRDWEGETYQCRVTHPHLPRALMRSTTASPGKRLAPEVMLPPSPEET 249				

illustrate the invention. The OSOSO protein contains an opossum CH2 IGE domain followed by a human CH3 IGE domain followed by an opossum CH2 IGE domain followed by a human CH3 IGE domain followed by an opossum CH4 IGE domain. The OSOSO-H protein also contains a C-terminal polyhistidine tag.

polypeptide sequence (e.g. an ORO polypeptide or an OSO polypeptide: CC ADN00643, ADN00646, ADN00650, ADN00652, ADN00654, ADN00656, ADN00658 or CC ADN00661). Administration of the composition to a mammal reduces the CC level of detectable free IgE in the mammal. The composition is useful for CC inducing an anti self-IgE antibody response in a mammal for treating or CC preventing allergies. The present sequence is an OSO protein, used to CC illustrate the invention. The modOSO-H protein contains an opossum CH2 CC IgE domain followed by a human CH3 IgE domain followed by an opossum CH4 CC IgE domain followed by a human CH3 IgE domain followed by an opossum CH4 CC IgE domain. The modOSO-H protein also contains point mutations in the CC human CH3 domains to abolish mast cell receptor binding and a C-terminal polyhistidine tag.

PT New composition comprising a self-IGE polypeptide and an aluminum
 PT compound, useful for inducing an anti self-IGE antibody response in a
 PT mammal for treating or preventing allergies.

XX XX

PS Claim 3; Fig 23; 102pp; English.

CC The present invention relates to a composition comprising a polypeptide
 CC and an aluminum compound, where the polypeptide comprises a self-IGE
 CC polypeptide sequence (e.g. an ORO peptide or an OSO polypeptide);
 CC ADN0643, ADN0645, ADN0650, ADN0654, ADN0656, ADN0658 or
 CC ADN0661). Administration of the composition to a mammal reduces the
 CC level of detectable free IGE in the mammal. The composition is useful for
 CC inducing an anti self-IGE antibody response in a mammal for treating or
 CC preventing allergies. The present sequence is H-OOC-H protein, used to
 CC illustrate the invention. The H-OOC-H protein contains an opossum CH2 IGE
 CC domain followed by a monkey CH3 IGE domain followed by an opossum CH4 IGE
 CC domain. The H-OOC-H protein also contains a N- and C-terminal
 CC polyhistidine tags.

XX Sequence 353 AA;

SO

Query Match 94.8%; Score 1759; DB 8; Length 353;
 Best Local Similarity 95.3%; Pred. No. 6.7-138;
 Matches 328; Conservative 3; Mismatches 11; Indels 2; Gaps 1;

QY 1 EPHHHHHHTSLPSEGPTVTLPPVVKLFISSCDPRGDASITOLCLVSGFSPAKVHTW 60
 Db 1 EPHHHHHHTSLPSEGPTVTLPPVVKLFISSCDPRGDASITOLCLVSGFSPAKVHTW 60
 QY 61 LVDGQEAEENLFPYTRPKREGGQTESLOQEVNTIQGMNSNTYCHVHNGSIFEDSSR 120
 Db 61 LVDGQEAEENLFPYTRPKREGGQTESLOQEVNTIQGMNSNTYCHVHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSYALSRSPSPDLFIRKSPPTICLVLAPSKGTVNLTMWSRASSKPVNHS 180
 Db 121 KCADSNPRGVSYALSRSPSPDLFIRKSPPTICLVLAPSKGTVNLTMWSRASSKPVNHS 180
 QY 181 RKEEKQRONGLTIVTSTLPVGTSTWDLEGTYQCRTYQHPLPRLMRSTKL--PGKRLAPE 238
 Db 181 RKEEKQRONGLTIVTSTLPVGTSTWDLEGTYQCRTYQHPLPRLMRSTKL--PGKRLAPE 238
 QY 181 ATGKEQRONGLTIVTSTLPVGTQDWLEGTYQCRTYQHPLPRLVRSMKTLASGKRLAPE 240
 Db 181 ATGKEQRONGLTIVTSTLPVGTQDWLEGTYQCRTYQHPLPRLVRSMKTLASGKRLAPE 240
 QY 239 VYMLPPSPPEETGTTRTVTCILRGFPSEISVQWLNNEEDHTGHHTTRPQDHGTDFP 298
 Db 241 VYMLPPSPPEETGTTRTVTCILRGFPSEISVQWLNNEEDHTGHHTTRPQDHGTDFP 300
 QY 299 FLYSRMLVNKSIWEKGNLVTCRVYHEALGSRTLEKSJHYSGN 342
 Db 301 FLYSRMLVNKSIWEKGNLVTCRVYHEALGSRTLEKSJHYSGN 342
 RESULT 15
 ID AAB06208 standard; protein; 341 AA.
 AC AAB06208;
 AC AAB06208 15
 DT 12-SEP-2003 (revised)
 DT 22-NOV-2000 (first entry)

XX DE Immunogenic peptide consisting of opossum CH2, dog CH3 and opossum CH4.
 XX KW Dog; opossum; immunoglobulin E; IGE; vaccination; infection; allergy;
 KW asthma; eczema; immunogenic peptide.
 XX OS Diapholphis virginiana.
 OS Canis sp.
 OS Chimeric.
 XX PN WO200025722-A2.
 XX PD 11-MAY-2000.
 XX PF 21-OCT-1999; 99WO-SE001896.

XX PR 02-NOV-1998; 98US-0106652P.
 PR 22-SEI-1999; 99US-0040636.
 XX (RESI-) RESISTENTIA PHARM AB.
 XX
 XX Hellman LT;
 XX WPI; 2000-365342/31.
 PT Immunogenic polypeptides useful for preventing the harmful effects of
 PT immunoglobulin E in mammals.
 PS Disclosure; Fig 2; 50pp; English.
 XX
 XX The present sequence is an immunogenic peptide consisting of the heavy
 CC chain constant regions 2 and 4 of the opossum IgE and the heavy chain
 CC constant region 3 from the dog. It was shown to cause a stronger
 CC polyclonal anti self IgE response than peptides consisting of the same
 CC regions from one mammal. Immunogenic peptides, particularly those
 CC consisting of different heavy chain constant regions, can be used for
 CC vaccination in humans, against bacterial and viral infections and
 CC allergies, such as asthma, fur, pollen and food allergies and eczema.
 CC (Updated on 12-SEP-2003 to standardize OS field)

XX Sequence 341 AA;

SQ Query Match 88.6%; Score 1644.5; DB 3; Length 341;
 Best Local Similarity 88.0%; Pred. No. 2.2e-128;
 Matches 301; Conservative 17; Mismatches 23; Indels 1; Gaps 1;

QY 1 EPHHHHHHTSLPSEGPTVTLPPVVKLFISSCDPRGDASITOLCLVSGFSPAKVHTW 60
 Db 1 EPHHHHHHTSLPSEGPTVTLPPVVKLFISSCDPRGDASITOLCLVSGFSPAKVHTW 60
 QY 61 LVDGQEAEENLFPYTRPKREGGQTESLOQEVNTIQGMNSNTYCHVHNGSIFEDSSR 120
 Db 61 LVDGQEAEENLFPYTRPKREGGQTESLOQEVNTIQGMNSNTYCHVHNGSIFEDSSR 120
 QY 121 KCADSNPRGVSYALSRSPSPDLFIRKSPPTICLVLAPSKGTVNLTMWSRASSKPVNHS 180
 Db 121 KCADSNPRGVSYALSRSPSPDLFIRKSPPTICLVLAPSKGTVNLTMWSRASSKPVNHS 180
 QY 181 RKEEKQRONGLTIVTSTLPVGTSTWDLEGTYQCRTYQHPLPRLMRSTKL--PGKRLAPE 238
 Db 181 RKEEKQRONGLTIVTSTLPVGTSTWDLEGTYQCRTYQHPLPRLMRSTKL--PGKRLAPE 238
 QY 181 ATGKEQRONGLTIVTSTLPVGTQDWLEGTYQCRTYQHPLPRLVRSMKTLASGKRLAPE 240
 Db 181 ATGKEQRONGLTIVTSTLPVGTQDWLEGTYQCRTYQHPLPRLVRSMKTLASGKRLAPE 240
 QY 239 VYMLPPSPPEETGTTRTVTCILRGFPSEISVQWLNNEEDHTGHHTTRPQDHGTDFP 298
 Db 241 VYMLPPSPPEETGTTRTVTCILRGFPSEISVQWLNNEEDHTGHHTTRPQDHGTDFP 300
 QY 299 FLYSRMLVNKSIWEKGNLVTCRVYHEALGSRTLEKSJHYSGN 342
 Db 301 FLYSRMLVNKSIWEKGNLVTCRVYHEALGSRTLEKSJHYSGN 342
 QY 301 YSRMLVNKSIWEKGNLVTCRVYHEALGSRTLEKSJHYSGN 342
 Db 300 YSRMLVNKSIWEKGNLVTCRVYHEALGSRTLEKSJHYSGN 342

Search completed: November 14, 2004, 14:58:12
 Job time : 167 secs

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ON protein - protein search, using sw model

Run on: November 14, 2004, 15:03:41 ; Search time 24 Seconds

(without alignments)
 945.032 Million cell updates/sec

Title: US-09-401-636-8

Sequence: 1 EFHHHHHHHTLSPLESQPVTL.....HEALPGSRTLEKSLHYHSAGN 342

Scoring table: BLOSUM62

Gapext 0.5

Searched: 478139 seqs, 66316000 residues

Total number of hits satisfying chosen parameters: 417130

Minimum DB seq length: 0
 Maximum DB seq length: 342Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgns_6/ptodata/1/iaa/5A_COMB.pep:
 2: /cgns_6/ptodata/1/iaa/5B_COMB.pep:
 3: /cgns_6/ptodata/1/iaa/6A_COMB.pep:
 4: /cgns_6/ptodata/1/iaa/6B_COMB.pep:
 5: /cgns_6/ptodata/1/iaa/PC7US_COMB.pep:
 6: /cgns_6/ptodata/1/iaa/backfile1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	579	31.2	113	2	US-09-232-539D-56
2	548.5	29.6	109	3	US-09-466-163B-1
3	548.5	29.6	109	4	US-09-802-096-1
4	548.5	29.6	109	4	US-09-802-077-1
5	538	29.0	106	2	US-08-232-539D-54
6	512	27.6	334	2	US-08-646-981-16
7	508	27.4	119	1	US-08-464-025A-1
8	501.5	27.0	331	2	US-08-646-981-17
9	490.5	26.4	118	3	US-08-466-151-1
10	490	26.4	333	1	US-08-436-163-6
11	490	26.4	333	1	US-08-024-253-6
12	476.5	25.7	329	4	US-09-313-342-12
13	476	25.6	327	2	US-08-761-377A-47
14	475.5	25.6	326	2	US-08-656-386-9
15	445.7	24.6	330	4	US-09-301-593-22
16	434	23.4	320	2	US-08-579-940-8
17	421.5	22.7	331	3	US-08-808-720-7
18	421.5	22.7	331	4	US-09-467-638-7
19	415.5	22.4	324	2	US-08-579-940-7
20	414	22.3	228	4	US-09-968-362A-27
21	411.5	22.2	218	4	US-09-483-388-7
22	411.5	22.2	229	4	US-09-968-362A-28
23	411.5	22.2	277	4	US-09-428-682B-30
24	411	22.1	253	4	US-09-428-682B-18
25	409	22.0	313	3	US-08-713-556F-36
26	408.5	22.0	217	4	US-09-483-388-5
27	408.5	22.0	283	4	US-09-854-864-9

Seq

RESULT 1
 US-08-232-539D-56
 ; Sequence 56, Application US/08232539D
 ; Patent No. 5955709
 ; GENERAL INFORMATION:
 ; APPLICANT: Presta, Leonard G.
 ; TITLE OF INVENTION: IgE Antagonists
 ; NUMBER OF SEQUENCES: 60
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94010
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/232, 539D
 ; FILING DATE: 21-09-1994
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/178583
 ; FILING DATE: 07-JAN-1994
 ; PRIOR APPLICATION DATA: 07/744768
 ; APPLICATION NUMBER: 07/744768
 ; FILING DATE: 14-AUG-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Svoboda, Craig G.
 ; REGISTRATION NUMBER: 39, 044
 ; REFERENCE DOCKET NUMBER: P0718P3
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1489
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 113 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-08-232-539D-56

Query Match Score 579; DB 2; Length 113;
 Best Local Similarity 98.2%; Pred. No. 1.3e-48;
 Matches 109; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy

122 CADSNPRGVSYILSRPSPFDFIRKSPTITLVVLDAPSKGTVNLTWSASGKPPVNHSTR 181

US-09-802-096-1

Ddb 1 CADDNPQRGSAYLSRPSPDLFIRKSPTITCLVVDLAPSKGKPVNHSSTR 60

Qy 182 KEEKQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKPG 232

Db 61 KEERQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKTSG 111

RESULT 2

US-08-466-163-B-1

Sequence 1, Application US/08466163B

GENERAL INFORMATION:

- APPLICANT: Jardieu, Paula M.
- ATTORNEY OR AGENT: Presta, Leonard G.
- TITLE OF INVENTION: Immunoglobulin Variants
- FILE REFERENCE: P0718P2C1D1
- CURRENT APPLICATION NUMBER: US/08/466,163B
- PATENT NO.: 6329109
- PRIOR FILING DATE: 1995-06-06
- PRIOR APPLICATION NUMBER: US 08/405,617
- PRIOR FILING DATE: 1995-03-15
- PRIOR APPLICATION NUMBER: US 08/185,899
- PRIOR FILING DATE: 1994-01-26
- PRIOR APPLICATION NUMBER: US 07/879,495
- PRIOR FILING DATE: 1992-05-07
- PRIOR APPLICATION NUMBER: US 07/744,768
- PRIOR FILING DATE: 1991-08-14
- NUMBER OF SEQ ID NOS: 64
- SEQ ID NO: 1
- LENGTH: 109
- ORGANISM: Homo sapiens
- TYPE: PRT

Query Match 29.6%; Score 548.5; DB 3; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45; Indels 1; Gaps 1;
Matches 106; Conservative 0; Mismatches 2;

Qy 124 DSNPQGVSYAISLRSPSPFDIFIRKSPTITCLVVDLAPSKGKPVNHSSTR 183

Db 1 DSNPQGVSYAISLRSPSPFDIFIRKSPTITCLVVDLAPSKGKPVNHSSTR 60

184 EKQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKPG 232

61 EKQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKTSG 108

RESULT 3

US-09-802-096-1

Sequence 1, Application US/09802096

GENERAL INFORMATION:

- APPLICANT: Jardieu, Paula M.
- ATTORNEY OR AGENT: Presta, Leonard G.
- TITLE OF INVENTION: Method of Preventing the Onset of Allergic Disorders (as amended)
- FILE REFERENCE: P0718P2C3US
- CURRENT APPLICATION NUMBER: US/09/802,096
- PATENT NO.: 6685399
- PRIOR FILING DATE: 2001-03-08
- PRIOR APPLICATION NUMBER: US 08/405,617
- PRIOR FILING DATE: 1995-03-15
- PRIOR APPLICATION NUMBER: US 08/185,899
- PRIOR FILING DATE: 1994-01-26
- PRIOR APPLICATION NUMBER: PCT/US92/06880
- PRIOR FILING DATE: 1992-08-14
- PRIOR APPLICATION NUMBER: US 07/879,495
- PRIOR FILING DATE: 1992-05-07
- PRIOR APPLICATION NUMBER: US 07/744,768
- NUMBER OF SEQ ID NOS: 64
- SEQ ID NO: 1
- LENGTH: 109
- ORGANISM: Homo sapiens
- TYPE: PRT

Query Match 29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45; Indels 1; Gaps 1;
Matches 106; Conservative 0; Mismatches 2;

Qy 124 DSNPQGVSYAISLRSPSPFDIFIRKSPTITCLVVDLAPSKGKPVNHSSTR 183

Db 1 DSNPQGVSYAISLRSPSPFDIFIRKSPTITCLVVDLAPSKGKPVNHSSTR 60

184 EKQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKPG 232

61 EKQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKTSG 108

RESULT 4

US-09-802-077-1

Sequence 1, Application US/09802077

GENERAL INFORMATION:

- APPLICANT: Jardieu, Paula M.
- ATTORNEY OR AGENT: Presta, Leonard G.
- TITLE OF INVENTION: Method of Treating Allergic Disorders (as amended)
- FILE REFERENCE: P0718P2C2US
- CURRENT APPLICATION NUMBER: US/09/802,077
- PATENT NO.: 6699472
- PRIOR FILING DATE: 2001-03-08
- PRIOR APPLICATION NUMBER: US 08/405,617
- PRIOR FILING DATE: 1995-03-15
- PRIOR APPLICATION NUMBER: US 08/185,899
- PRIOR FILING DATE: 1994-01-26
- PRIOR APPLICATION NUMBER: PCT/US92/06880
- PRIOR FILING DATE: 1992-08-14
- PRIOR APPLICATION NUMBER: US 07/879,495
- PRIOR FILING DATE: 1992-05-07
- PRIOR APPLICATION NUMBER: US 07/744,768
- PRIOR FILING DATE: 1991-08-14
- NUMBER OF SEQ ID NOS: 64
- SEQ ID NO: 1
- LENGTH: 109
- ORGANISM: Homo sapiens
- TYPE: PRT

Query Match 29.6%; Score 548.5; DB 4; Length 109;
Best Local Similarity 97.2%; Pred. No. 1.1e-45; Indels 1; Gaps 1;
Matches 106; Conservative 0; Mismatches 2;

Qy 124 DSNPQGVSYAISLRSPSPFDIFIRKSPTITCLVVDLAPSKGKPVNHSSTR 183

Db 1 DSNPQGVSYAISLRSPSPFDIFIRKSPTITCLVVDLAPSKGKPVNHSSTR 60

184 EKQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKPG 232

61 EKQNGTILTVTSTLPVGTRDIEGETYQCRVTHPHLPRALMRSSTKTSG 108

RESULT 5

US-08-232-539D-54

Sequence 54, Application US/08232539D

GENERAL INFORMATION:

- APPLICANT: Presta, Leonard G.
- ATTORNEY OR AGENT: Jardieu, Paula M.
- TITLE OF INVENTION: IgE Antagonists
- NUMBER OF SEQUENCES: 60
- CORRESPONDENCE ADDRESS:
- ADDRESSEE: Genentech, Inc.
- STREET: 1 DNA Way
- CITY: South San Francisco
- STATE: California
- COUNTRY: USA
- ZIP: 94080
- COMPUTER READABLE FORM:

TYPE: PRT

ORGANISM: Homo sapiens

NUMBER OF SEQ ID NOS: 64

LENGTH: 109

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Warpatic (Genentech)

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/232,539D
 FILING DATE: 21-Apr-1994
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 0B/178583
 FILING DATE: 07-JAN-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/144768
 FILING DATE: 14-AUG-1991.
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REFERENCE/DOCKET NUMBER: 39-044
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/522-1489
 TELEFAX: 650/522-9881
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 106 amino acids
 TYPE: Amino Acid
 TOPOLogy: Linear
 US-08-232-539D-54

Query Match 6 29.0%; Score 538; DB 2; Length 106;
 Best Local Similarity 98.0%; Pred. No. 1.le-4%; Indels 0; Gaps 0;
 Matches 102; Conservative 0; Mismatches 2;

Qy 129 GVSAYLRSRSPFDLIRKSPITICLVVLDLAPSKGTVNLTVASGRKVNHSTRKEKORN 188
 Db 1 GVSAYLRSRSPFDLIRKSPITICLVVLDLAPSKGTVNLTVASGRKVNHSTRKEKORN 60

Qy 189 GTLTIVTSTLPVGCTTDWIEBEETYQCRVTHPLPALARSTTKLPG 232
 Db 61 GTLTIVTSTLPVGTRDWIEGETYQCRVTHPLPALARSTTKLPG 104

RESULT 6
 US-08-646-981-16
 Sequence 16, Application US/08646981
 Patent No. 5852183
 GENERAL INFORMATION:
 APPLICANT: MAEDA, HIROAKI
 APPLICANT: EDA, YASUYUKI
 APPLICANT: KIMACHI, KAIZUHIKO
 APPLICANT: ONO, YOICHI
 APPLICANT: TOKIYOSHI, SACHIO
 TITLE OF INVENTION: DOG-MOUSE HETERHYBRIDOMA AND GENE
 TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
 TITLE OF INVENTION: IMMUNOGLOBULINS
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 STREET: PO BOX 747
 CITY: FALLS CHURCH
 STATE: VA
 COUNTRY: USA
 ZIP: 22040-0747

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.30
 CURRENT APPLICATION DATA:
 FILING DATE:
 APPLICATION NUMBER: US/08/646,981
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: WEINER, MARC S

REGISTRATION NUMBER: 32,181
 REFERENCE/DOCKET NUMBER: 1488-106
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 334 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: Peptide
 US-08-646-981-16

Query Match 7 27.6%; Score 512; DB 2; Length 334;
 Best Local Similarity 35.9%; Pred. No. 2.1e-12%; Indels 38; Gaps 12;
 Matches 122; Conservative 60; Mismatches 122;

Qy 23 PTVKLFHSSCDPRAHSTIQLLCLVSGFSPARKVHTW----LVDGQAENLPPYTRPK 78
 Db 5 PSVFLDPSCG--STSGSTVALALLSGXYPEPTVSNMSGSLTG-----VHTFSD 55

Qy 79 REGGGDTFSLOSEVNNTIGQWMSNTTYCHVKH-----NGSIFE--DSSRK 121
 Db 56 LQSSSILYSLSSMTPVSSSW-SSSETFTCNVAHPASKTRVTDKPVKRENGRVRPPDCPK 114

Qy 122 CADSNPRGYSAYLSRSPSPD-LFIRKSPNITCLYDLAPSKGTVNLTVASGRKVNH- 179
 Db 115 PAPENMIGGPSPVFIFPKPKDTLIARTPAVTCVVDLGEDPEVQISWF-VDGKQMQPAK 173

Qy 180 TRKEEKORNGTLTSTLPLVGTROMIEGETYQCRVTHPLPALARSTTKLPGKRLAPEV 239
 Db 174 TQPREEOFNTYRVSVLPLVGHQWLKGKQFTCKVNNKALPSPIERTISKARGQAHQPSV 233

Qy 240 YMLPPSPPEE-TGTTATVTCUJRGYPSEETSVQWLENEBDHTGHHTTRPOKDHGTDSPF 298
 Db 234 YVLPSREELSKNTVSLTCLIKDPPPDIVQNSQQEPESKRTTPQOLDE-DGSY 291

Qy 299 FLYSRMLVNKNSIWEKGNYLTCRVTYHEALPGCSRTEKSHYSAG 341
 Db 292 FLYSKUSVDKSRWQGDTFICAVNHEALHNHYT-QKSLSHSPG 333

RESULT 7
 US-08-464-025A-1

Sequence 1, Application US/08464025A
 Patent No. 5594514
 GENERAL INFORMATION:
 APPLICANT: Jardieu et al.
 TITLE OF INVENTION: IMMUNOGLOBULIN VARIANTS
 NUMBER OF SEQUENCES: 27
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genentech, Inc.
 STREET: 1 DNA Way
 CITY: South San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94080
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WinPat-in (Genentech)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/464,025A
 FILING DATE: 05-Jun-1995
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Svoboda, Craig G.
 REGISTRATION NUMBER: 39,044
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-1489
 TELEX/FAX: 650/952-3881
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08-464-025A-1

Query Match 27.4%; Score 500; DB 2; Length 119;
 Best Local Similarity 88.9%; Pred. No. 1..le-41;
 Matches 104; Conservative 1; Mismatches 4; Indels 8; Gaps 4;

Qy 124 DSNPGVSAVLRSRSPFDLFIKSPTITCLVVDLAPSRTGTVNLTWRSRAS--GKPVNHS 179
 Db 2 DSNPGVSAVLRSRSPFDLFIKSPTITCLVVDLAPSRTGTVNLTWRSRAS--GKPVNHS 61

Qy 180 TRKEEKQR--NGTLTVTSTLPVGTRDWTGEGTYQCRTYHPLPRL-MRSTTKLPG 232
 Db 62 TRKEEKQRKXKGTLVTSTLPVGTRDWTGEGTYQCRTYHPLPRLXMRSTTKTSG 188

RESULT 8
 US-08-646-981-17
 / Sequence 17, Application US/08646981
 / Patent No. 5852.83
 / GENERAL INFORMATION:
 / APPLICANT: MAEDA, HIROAKI
 / APPLICANT: EDA, YASUOKI
 / APPLICANT: KIMACHI, KAZUHIKO
 / APPLICANT: ONO, YOICHI
 / APPLICANT: TOKIYOSHI, SACHIO
 / TITLE OF INVENTION: DOG- MOUSE HETEROHYBRIDOMA AND GENE
 / TITLE OF INVENTION: FRAGMENT CODING FOR CONSTANT REGION OF CANINE
 / NUMBER OF SEQUENCES: 17
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 / STREET: PO BOX 747
 / CITY: FALLS CHURCH
 / STATE: VA
 / ZIP: 22040-0747
 / COMPUTER READABLE FORM:
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: PatentIn Release #1.0, Version #1.30
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/646,981
 / FILING DATE:
 / CLASSIFICATION: 435
 / ATTORNEY/AGENT INFORMATION:
 / NAME: WEINER, MARC S
 / REGISTRATION NUMBER: 32,181
 / REFERENCE/DOCKET NUMBER: 1488-106
 / INFORMATION FOR SEQ ID NO: 17:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 331 amino acids
 / TYPE: amino acid
 / STRANDEDNESS: single
 / TOPOLOGY: linear
 / MOLECULE TYPE: peptide

US-08-646-981-17

Query Match 27.0%; Score 501.5; DB 2; Length 331;
 Best Local Similarity 36.3%; Pred. No. 2.2e-10;
 Matches 122; Conservative 62; Mismatches 125; Indels 12; Gaps 12;

Qy 23 PTYKLFISSCDPRGDAHSTIQCLCVSGFSPAKVHTWLDGQEAEENLPPFTTRPKREGG 82
 Db 5 PSVFLPLAPSCG--STGCGTSLACLYSGFPEPPTVSW-NISGLTSLGVHTFPSPVLSKSSG- 60

Qy 83 QTFSLQSEVNNTQGMNSNTYCHVKHNS-----FEDSSRKCADSNP---RG 129
 Db 61 -LYSSLSSMVTYFSSR-LPSEFTCTNVHPATNTKVDKPGVPEKSTCKC1SPCPVPEPSLGG 118

RESULT 9
 US-08-466-151-1
 / Sequence 1, Application US/08466151
 / Patent No. 603743
 / GENERAL INFORMATION:
 / APPLICANT: Jardieu, Paulia M.
 / APPLICANT: Presta, Leonard G.
 / TITLE OF INVENTION: Immunoglobulin Variants
 / NUMBER OF SEQUENCES: 65
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Genentech, Inc.
 / STREET: 1 DNA Way
 / CITY: South San Francisco
 / STATE: California
 / COUNTRY: USA
 / ZIP: 94080
 / COMPUTER READABLE FORM:
 / COMPUTER: IBM PC compatible floppy disk
 / MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WinPptin (Genentech)
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08/466,151
 / FILING DATE:
 / CLASSIFICATION:
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/466163
 / FILING DATE: 06-Jun-1995
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: WinPptin (Genentech)
 / PRIORITY DATA:
 / APPLICATION NUMBER: 08/1405617
 / FILING DATE: 15-MAR-1995
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/185899
 / FILING DATE: 26-JAN-1994
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 08/1405617
 / FILING DATE: 07-MAY-1992
 / PRIOR APPLICATION DATA:
 / APPLICATION NUMBER: 07/744768
 / FILING DATE: 14-AUG-1991
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Surooda, Craig G.
 / REGISTRATION NUMBER: 39,044
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: 650/25-1489
 / TELEFAX: 650/952-5881
 / INFORMATION FOR SEQ ID NO: 1:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 118 amino acids
 / TYPE: Amino Acid
 / TOPOLOGY: Linear
 US-08-466-151-1

Query Match 26.4%; Score 490.5; DB 3; Length 118;
 Best Local Similarity 88.0%; Pred. No. 5.5e-40;
 Matches 103; Conservative 1; Mismatches 9; Gaps 5;

RESULT 12
 US-09-313 942-12
 Sequence 12, Application US/09313942
 Patent No. 6472179
 GENERAL INFORMATION:
 APPLICANT: REGENERON PHARMACEUTICALS, INC.
 TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING
 FILE REFERENCE: REG 203-A
 CURRENT APPLICATION NUMBER: US/09/313, 942
 PELTOR APPLICATION NUMBER: 09/13, 942
 PRIOR FILING DATE: 1999-05-19
 PRIORITY APPLICATION NUMBER: 60/101, 858
 PRIORITY FILING DATE: 1998-09-25
 SOFTWARE: FastSEQ for Windows Version 3.0
 SEQ ID NO: 12
 LENGTH: 329
 TYPE: PROT
 ORGANISM: Homo sapiens
 US-09-313-942-12

Query Match 25.7%; Score 476.5; DB 4; Length 329;
 Best Local Similarity 35.5%; Prod. No. 5.8e-38; Matches 122; Conservative 58; Mismatches 131; Indels 33; Gaps 12;

Qy 15 SGPYTIIPPTVKLPHSSCDPRGDAHSTIQLLCLVSGSPAKTVW---LVDGQAENL 70
 Db 1 SGASTKGPRGVFPL--APCS-RSTSESTAALGLCIVKDIFPEPPTVSNNSGALTSG---VHT 54
 Qy 71 FPYITRPRKEGGQTFSLOSEVNITQGMNSNTYCHVKGNSIFEDSSRKCADSNP--- 127
 Db 55 FPAVL---QSSGYLSLSSSVTPVSSS-LGKTKYTNCVUDKPSNTVTDKRVESKYGPCCP 109
 Qy 128 -----RGVAYLRSRSPFD-LFIRKSPITCLVYDLPASKGTYNLTWSRASGRKPVNH 178
 Db 110 SCAPEFLGGPSVFLPPKPKUTLMIIRTPEVICVUVDVSQEDPEVQFNWVVDGVEVNA 169
 Qy 179 STRKEEKORGNTLTVTSTLPGVTRDWEGETYQCRTYHPLPRLMRSTKLPGKRLAPE 238
 Db 170 KTRPREEQNSTYRVVSVLTVHQDWNGKEYCKVSKNKGDPSSIEKTISAKGQPREPQ 229

Qy 239 VMLPPSPSE-TGTTTVCYLRGFYDSEISYQWLNNEEDHTGHHTTRPQDKHGTDS 297
 Db 230 VTLPPSPQEMTNQVSITCLYKGFYSDIAEWENGQPN-NYKTTPPVLD--SDGSS 285

Qy 298 FELYSRMLVYKTSWEKGNLVTCRVLVHEALPGSRTLEKSLHYSG 341
 Db 286 FLYSLRITVDSRQEGNFSVMEALHNHYT-QKSLSLSG 326

GENERAL INFORMATION:
 APPLICANT: Denney Jr., Dan W.
 TITLE OF INVENTION: Vaccines For Treatment Of Lymphoma And Leukemia
 NUMBER OF SEQUENCES: 80
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Medlen & Carroll, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California
 COUNTRY: United States Of America
 ZIP: 94104
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/761,277A
 FILING DATE: 06-DEC-1996
 CLASSIFICATION: 44
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/644,664
 FILING DATE: 01-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Macknight, Kaurin T.
 REGISTRATION NUMBER: 38,230
 REFERENCE/DOCKET NUMBER: GENITOPE-02406
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 705-8410
 TELEFAX: (415) 397-5338
 INFORMATION FOR SEQ ID NO: 47:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 327 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-761-277A-47

Query Match 25.6%; Score 476; DB 2; Length 327;
 Best Local Similarity 35.8%; Prod. No. 6.5e-38; Matches 116; Conservative 57; Mismatches 122; Indels 30; Gaps 10;

Qy 35 RGDANHSTIOLCLVSGSPAKTVW---LVDGQAENLFPYTTRKREGQQTFSIQS 90
 Db 16 RSTSESTAALGLCIVKDIFPEPPTVSNNSGALTSG---VHTFAVL---QSSGLYSSV 68
 Qy 91 VNTIQGMNSNTVTCHYGHNSLFEDSSRKCADSNP-----RGVAYLSSRSP 139
 Db 69 VTYPSSS-LGKTKYTNCVUDKPSNTVTDKRVESKYGPCCP 127
 Qy 140 FD-LFIRKSPITCLVYDLPASKGTYNLTWSRASGRKPVNHSTRKEEKORGNTLTSTLP 198
 Db 128 KDILMISRTPPEVTCVUVDVSQEDPEVQFNWVVDGVEVNA 169
 Qy 199 VGTDRWEEBTYCRVTHPLPRLMSTKLPGKRLAPEYMLPPEPE-TGTTRVTC 257
 Db 188 VLHDWLNGKEYCKVSKNKGDPSSIEKTISAKGQPREPQ 247

Qy 258 LIRGFYPSISYQWLNNEEDHTGHHTTRPQDKHGTDSFSELYSMVNSIWEKGNLV 317
 Db 248 LVFGFYPSPDIAVEWESNCOPEN-NYKTTPPVLD--SDGSS 303

Qy 318 TCRVVAEALPGSRTLEKSLHYSG 341
 Db 304 SC5VMEAHNNHYT-QKSLSLSG 326

RESULT 14
 US-08-656-586-9
 ; Sequence 9, Application US/08656586
 ; Patent No. 5834597
 ; GENERAL INFORMATION:

APPLICANT: Tso, J. Yun
 APPLICANT: Cole, Michael S.
 APPLICANT: Anasetti, Claudio
 TITLE OF INVENTION: Mutated No. 5834397activating IgG2 Domains and
 NUMBER OF SEQUENCES: 13
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Software #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/656, 586
 FILING DATE: 31-MAY-1996
 CLASSIFICATION: 530
 ATTORNEY/AGENT INFORMATION:
 NAME: Liebeschutz, Joseph O.
 REGISTRATION NUMBER: 37,505
 REFERENCE/DOCKET NUMBER: 11823-007210US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 SEQUENCE INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 326 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 FEATURE:
 NAME/KEY: Protein
 LOCATION: 1..326
 OTHER INFORMATION: /note= "heavy chain constant region of
 IgG2 mutant 3"
 US-08-656-586-9

Query Match 25.6%; Score 475.5; DB 2; Length 326;
 Best Local Similarity 35.8%; Pred. No. 7.2e-18;
 Matches 115; Conservative 57; Mismatches 120; Indels 29; Gap 35

Qy 35 RGDAHSTIQILQCLIVSGFSPAKVHYTNV---LVDGQEAENLPPYTRKREGQTQTSIQ
 Db 16 RSTSESTAALGCLVQDVFPEPVTVNSGATSG--VHTFPAVL--QSSGLYSI
 Qy 91 VNIUTQQGWMSSNTYTCVYKH--NGS1FEDSSRKCADSNP----RCVGSAYLRSRPS
 Db 69 VTVPPSNF-GTQTYTCVNDHKPSNTVKDVTYKVERKCCVCPAPPAAAPSVELFPKK
 Qy 141 D-LFIRKSPTITOLVYDAPSIGTVNLWRSAGSKPVNHSITKEEKORGNTIVTSTI
 Db 128 DTLMISRTPEVTCVWVDSHDEPEVQFMWVYDGEVENAKTKPREEQFNSTRVVSVYL
 Qy 200 GTRDWIPIETVYCCRVTPHFLPRALMRSTTKLPKRLADEVYMLPPSPBE-TGTTRVTV
 Db 188 VHQDWLNKEYKCVSNKGGLPAPIEKTISKTGQPREGVYTLPPSREMTKRNQVSU
 Qy 259 IRGFYPSSPSISQWLFNNEDHTGHHTTRPQDHDGTDSEFLYSRMLVJNKSIWEKGNI
 Db 248 VKGFYPSDIAVENEWSNGOPEN-NYKTFPPMLD-SDSFFFLYSKLTVDKSRWQGNTI
 Qy 319 CRVHEALPGSRPLTEKSHYS
 Db 323 CSMHEALHNHYT-OKSLSL

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US-09-301-593-22 ; Sequence 22, Application US/09301593A
; Sequence No. 6455677 ; Patent No. 6455677
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pitjar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: PAP-specific Antigen
; FILE REFERENCE: 0652-1890001
; CURRENT APPLICATION NUMBER: US/09/301593-22
; CURRENT FILING DATE: 1999-04-29
; EARLIER APPLICATION NUMBER: EP 981071
; EARLIER FILING DATE: 1998-04-30
; EARLIER APPLICATION NUMBER: US 60/0818
; EARLIER FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 22
LENGTH: 330
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-22

Query Match 24.6% Score
Best Local Similarity 34.7% Prd.
Matches 118; Conservative 56; Mi

Qy      22 PPTVKLFSSCDRQDAHSTIQLC
Db       6 PSYPLAPSSKSKTSG---GTAAGC
Qy      78 KREGGQTFLQSEBVNTIQGQWMSNN
Db       58 - QSSGAYLSSVVTVPSSS-LGTQ
Db     124 DSNPGRVSAYLSRPBSPF-LFIRKS
Db     115 PELLGPSVFLPPKPKDFTLMISRT
Qy      183 EEKONGTLYTVTSPFLPVGTRDWIG
Db     175 REEQNSTRVSVTIVHQDWING
Db     243 PPSPBE-TGTTTRTVTCLIRGPYPSE
Db     235 PPSREMTKNOVSITCLVRKGFPYHEAL
Qy      302 SRMLVTKNSIWEKGNIWTCRVWHEAL
Db     291 SKLTDKSRMWOQGNWFSCSYMWHEAL

Search completed: November 14, 2004, 15
Job time : 25 secs

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Job time : 25 secs

RESULT 15

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